

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 21:10:28 ; Search time 11 Seconds

(without alignments)
222.464 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59

Sequence: 1 KYHSLARAGKVRGQTPKVA.....RRFVNVPTFGKKKGPNANS 59

Scoring table: OLIGO

Searched: 112892 segs, 41476328 residues

Word size : 0

Total number of hits satisfying chosen parameters: 112892

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : SwissProt_40.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	59	RS30_HUMAN	Q05472 homo sapien
2	22	37.3	62	RS30_ARATH	P49689 arabidopsis
3	18	30.5	59	RS30_ORYLA	O9W6Y0 oryzias lat
4	12	20.3	58	RS30_PLAFA	O96269 plasmodium
5	12	20.3	61	RS30_SCHPO	O42952 schizosach
6	12	20.3	62	RS30_YEAST	O12087 saccharomyc
7	11	18.6	11	RS30_ONCMY	P83328 oncorhynchu
8	7	11.9	133	HNS_PROVU	P18818 proteus vul
9	7	11.9	346	YOC2_CAEEL	O09261 caenorhabd1
10	7	11.9	489	COLB_HUMAN	O9hr76 homo sapien
11	7	11.9	1254	POLS_EEYVM	P36321 venezuelan
12	6	10.2	78	R27A_DICDI	P14797 dictyostell
13	6	10.2	78	RS18_BACSU	P21475 bacillus su
14	6	10.2	80	EXS5_VIBCH	O9Kt11 vibrio chol
15	6	10.2	105	YGRM_MICEC	P24621 micromonosp
16	6	10.2	105	YGRM_MICEC	P24621 micromonosp
17	6	10.2	123	RL19_TREPA	O83879 treponema p
18	6	10.2	125	RS25_HUMAN	P25111 homo sapien
19	6	10.2	127	RS11_RICPR	O9ZCS8 rickettsia
20	6	10.2	128	YQ82_CAEEL	O09237 caenorhabd1
21	6	10.2	130	YNO3_YEAST	P53908 saccharomyc
22	6	10.2	137	YKDI_YEAST	P36098 saccharomyc
23	6	10.2	142	RS16_CANAL	O94017 candida alb
24	6	10.2	142	RS16_YEAST	P40213 saccharomyc
25	6	10.2	157	ENDY_BP74	P13340 bacterioph
26	6	10.2	167	YK20_YEAST	O25278 leishmania
27	6	10.2	175	RL14_LEIDO	O25278 leishmania
28	6	10.2	178	FXYS_MOUSE	P97808 mus musculu
29	6	10.2	188	CC42_CAEEL	O05062 caenorhabd1
30	6	10.2	188	RASK_MEIGA	P79800 meleagris g
31	6	10.2	195	PAPR_ECOLI	P07111 escherichia
32	6	10.2	195	PRSH_ECOLI	P42185 escherichia
33	6	10.2	198	RMRP_YEAST	P40993 saccharomyc

ALIGNMENTS

RESULT 1					ALIGNMENTS				
ID	RS30_HUMAN	STANDARD:	PRT:	59 AA.					
AC	O05472; 095261;								
DT	01-JUN-1994 (Rel. 29, Created)								O14807 homo sapien
DT	01-JUN-1994 (Rel. 29, Last sequence update)								O08989 mus musculu
DT	16-OCT-2001 (Rel. 40, Last annotation update)								P97538 ratus norv
DE	40S ribosomal protein S30.								P57212 buchiera ap
GN	FAU.								P06780 saccharomyc
OS	Homo sapiens (human),								P24536 burkholderi
OS	Mus musculus (mouse),								P38978 hydra atten
OS	Rattus norvegicus (Rat),								P35536 bacillus su
OS	Cricetulus griseus (Chinese hamster), and								P57280 buchiera ap
OS	Sus scrofa (Pig).								O8ZC21 pyrobaculum
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;								P47006 saccharomyc
OC	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.								O94051 caenorhabd1
OX	NCBI_Taxid:9606, 10090, 10116, 10029, 9823;								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human;								
RX	MEDLINE=92412144; PubMed=1326960;								
RA	Kas K., Michiels L., Merregaert J.;								
RT	"Genomic structure and expression of the human fau gene: encoding the								
RL	ribosomal protein S30 fused to a ubiquitin-like protein.";								
RN	Biochem. Biophys. Res. Commun. 187:927-933(1992).								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Human, and Mouse;								
RX	MEDLINE=93368957; PubMed=8395683;								
RA	Michiels L., van der Raaijlaert E., van Hasselt F., Kas K.,								
RT	Merregaert J.;								
RL	"fau cDNA encodes a ubiquitin-like-S30 fusion protein and is								
RT	expressed as an antisense sequence in the Finkel-Biskis-Reilly murine								
RL	sarcoma virus.";								
RN	Oncogene 8:2537-2546(1993).								
RP	SEQUENCE FROM N.A., AND SEQUENCE OF 1-18.								
RC	SPECIES=rat; STRAIN=Sprague-Dawley; TISSUE=liver;								
RX	MEDLINE=93352612; PubMed=8394356;								
RA	Olvera J., Wool I.G.;								
RT	"The carboxyl extension of a ubiquitin-like protein is rat ribosomal								
RL	protein S30.";								
RN	J. Biol. Chem. 268:17967-17974(1993).								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Mouse; STRAIN=BA1B/c;								
RX	MEDLINE=95241522; PubMed=7724584;								
RA	Nakamura M., Xavier R.M., Tsunematsu T., Tanigawa Y.;								
RT	"Molecular cloning and characterization of a cDNA encoding monoclonal								
RL	non-specific suppressor factor.";								
RN	Proc. Natl. Acad. Sci. U.S.A. 92:3463-3467(1995).								
RP	SEQUENCE FROM N.A.								
RC	SPECIES=Mouse; STRAIN=BA1B/c; TISSUE=liver;								
RX	MEDLINE=95293388; PubMed=7774934;								
RA	Castels D., Poltler C., Guenet J.-L., Merregaert J.;								

RT "The mouse Fau gene: genomic structure, chromosomal localization, and
 RT characterization of two retropseudogenes."
 RL Genomics 25:291-294(1995).
 RN [6]
 RP SEQUENCE FROM N.A.
 RC SPECIES=C.griseus;
 RA Rossmann T.G., Wang Z.;
 RL Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC SPECIES=Pig; TISSUE=uterus;
 RA MEDLINE=9724440; PubMed=9089280;
 RA Chetzoif S., D'Andrea S.;
 RT "Diquitin is physiologically induced by interferons in luminal
 RT epithelium of porcine uterine endometrium in early pregnancy: global
 RT RT-PCR cDNA in place of RNA for differential display screening";
 RL FEBS Lett. 405:148-152(1997).
 CC -1 MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
 CC C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBQUITIN-LIKE PROTEIN.
 CC -1 SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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 DR EMBL: X65921: CAA46714.1; ALT_INIT.
 DR EMBL: X65923: CAA46716.1; ALT_INIT.
 DR EMBL: X62671: CAA44546.1; -
 DR EMBL: X62671: CAA44545.1; ALT_INIT.
 DR EMBL: X65922: CAA46715.1; ALT_INIT.
 DR EMBL: D26610: BAA05655.1; ALT_INIT.
 DR EMBL: L33715: AAA91564.1; ALT_INIT.
 DR EMBL: U41499: AAA83776.1; ALT_INIT.
 DR EMBL: U72543: AAB52915.1; ALT_INIT.
 DR PIR: JCI278; JCI278.
 DR Genew: HGNC:3597; FAU.
 DR MIM: 134690; -
 DR MGD: MGI:102547; Fau.
 DR RIBOSOMAL PROTEIN.
 DR KW
 SQ SEQUENCE 59 AA; 6648 MW; 012AC1FB55B01A4 CRC64;
 QY 1 KVGSLARAGKVGQTPPKVAKQKKKKTKGRARRMQYNRRFVNVVPTFGKKKGPVANS 59
 DB 1 KVGSLARAGKVGQTPPKVAKQKKKKTKGRARRMQYNRRFVNVVPTFGKKKGPVANS 59
 ID RS30_ARATH STANDARD; PRT; 62 AA.
 AC P49689; 082203; Q9MOEA;
 DT 01-FEB-1996 (Rel. 33. Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S30.
 GN (RPS30A OR ATG219750 OR F6F22.22) AND
 GN (RPS30B OR ATG29390 OR F17A13.210) AND
 GN (RPS30C OR ATG56670 OR MIK19.12).
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eustosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBL_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=cv. Columbia;

RA Lebas M., Regad F., Lescure B.;
 RL Submitted (OCT-1993) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A. (RPS30A).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083487; PubMed=10617197;
 RA Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,
 RA Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,
 RA Bueli C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H.L.,
 RA Moffat K.S., Cronin L.A., Shen M., Pal G., Van Aken S., Umeyam L.,
 RA Tallon L.J., Gill J.E., Adams M.D., Carreira A.J., Creasy T.H.,
 RA Goodman H.M., Somerville C.R., Copenhaver G.P., Preuss D.,
 RA Nierman W.C., White O., Eisen J.A., Salzberg S.L., Fraser C.M.,
 RA Venter J.C.;
 RT "Sequence and analysis of chromosome 2 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:761-768(1999).
 RN [3]
 RP SEQUENCE FROM N.A. (RPS30B).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=20083488; PubMed=10617198;
 RA Meyer K.F.X., Schueller C., Wambutt R., Murphy G., Volckaert G.,
 RA Pohl T., Duesterhoeft A., Stiekema W., Entian K.-D., Terry N.,
 RA Harris B., Ansoorge W., Brandt P., Grivall L.A., Rieger M.,
 RA Weichselgartner M., de Simone V., Obermaier B., Mache R., Mueller M.,
 RA Kreis M., Delseny M., Puigdomenech P., Watson M., Schmidtheinl T.,
 RA Reichert B., Portetelle D., Perez-Alonso M., Boutry M., Bancroft I.,
 RA Vos P., Hohenseil J., Zimmermann W., Weller H., Ridley P.,
 RA Langham S.-A., McCullagh B., Bilham L., Robben J.,
 RA Van der Schuren J., Grymonprez B., Chuang Y.-J., Vandenbussche F.,
 RA Braeken M., Weltjens I., Voet M., Bastiaens I., Aert R., Defoer E.,
 RA Weltenegger T., Bothe G., Rampsperger U., Hilbert H., Braun M.,
 RA Holzner E., Brandt A., Peters S., van Staveren M., Dirke W.,
 RA Moilman P., Klein lankhorst R., Rose M., Hauf J., Koester P.,
 RA Bernseiser S., Hempel S., Feldpausch M., Lambert R., Van den Daele H.,
 RA De Keyser A., Buyschaert C., Gielen J., Villarroel R., De Clercq R.,
 RA Van Montagu M., Rogers J., Cronin A., Quail M., Bray-Allen S.,
 RA Clark L., Doggett J., Hall S., Kay M., Lennard N., McIay R., Mayes R.,
 RA Petlet A., Rajandream M.A., Lyne M., Benes V., Rechmann S.,
 RA Borkova D., Bloeker H., Scharfe M., Grimm M., Loehner T.-H.,
 RA Dose S., de Haan M., Maarse A.C., Schaefer M., Mueller-Auer S.,
 RA Gabel C., Fuchs M., Faltmann B., Grandert K., Plavandi A.,
 RA Neumann S., Argirou A., Vitale D., Ligouri K., Dauner D., Herzi A.,
 RA Massenet O., Quigley F., Clabaud G., Muendlein A., Felber R.,
 RA Schnabl S., Hiller R., Schmidt W., Lecharny A., Aubourg S.,
 RA Chetdor F., Cooke R., Berger C., Montfort A., Casacuberta E.,
 RA Gibbons T., Weber N., Vandenbol M., Barges M., Terol J., Torres A.,
 RA Perez-Perez A., Purnelle B., Bent E., Johnson S., Tacon D., Jesse T.,
 RA Heijnen L., Schwarz S., Scholler P., Heber S., Francis P., Bleike C.,
 RA Friseman D., Haase D., Lemcke K., Mewes H.-W., Stocker S.,
 RA Zaccaria P., Bevan M., Wilson R.K., de la Bastide M., Habermann K.,
 RA Parnell L., Dedha N., Gnoj L., Schut K., Huang E., Spiegel L.,
 RA Sekhon M., Murray J., Sheat P., Cordes M., Abu-Threideh J.,
 RA Stoeneking T., Kalicki J., Graves T., Harmon G., Edwards J.,
 RA Latreille P., Courtney L., Cloud J., Abbott A., Scott K., Johnson D.,
 RA Minx P., Bentley D., Fulton B., Miller N., Greco T., Kemp K.,
 RA Kramer J., Fulton L., Mardis E., Dante M., Pepin K., Hillier L.,
 RA Nelson J., Spieth J., Ryan E., Andrews S., Geisel C., Layman D.,
 RA Du H., Ali J., Berghoff A., Jones K., Dione K., Cotton M., Joshi C.,
 RA Antonoli B., Zidanic M., Strong C., Sun H., Lamar B., Yordan C.,
 RA Ma P., Zhong J., Preston R., Vill D., Shekher M., Matero A., Shah R.,
 RA Swaby I.K., O'Shaughnessy A., Rodriguez M., Hoffman J., Gill S.,
 RA Gravat S., Shohdy N., Hasegawa A., Rodriguez M., Hoffman J., Gill S.,
 RA Chen E., Maria M., Martienssen R., McCombie W.R.;
 RT "Sequence and analysis of chromosome 4 of the plant Arabidopsis
 RT thaliana";
 RL Nature 402:769-777(1999).
 RN [4]
 RP SEQUENCE FROM N.A. (RPS30C).
 RC STRAIN=cv. Columbia;
 RX MEDLINE=98403884; PubMed=9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miya Jima N.,
 RA Tabata S.;

RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN-CV, Columbia;
 RA Shinozaki K., Davis R.W., Ecker J.R., Theologis A.;
 RT "RKEN Arabidopsis full length cDNA clones (RnFLs) sequenced by the
 RT SSP consortium (Salk/Stanford/PGSC).";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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 DR EMBL: Z26869; CAAB1482.1; -;
 DR EMBL: AC005169; AAC62141.2; -;
 DR EMBL: AL161574; CAB79697.1; -;
 DR EMBL: AL096692; -; NOT_ANNOTATED_CDS.
 DR EMBL: AB013392; BAB09885.1; -;
 DR EMBL: AY052341; AAK96533.1; -;
 DR EMBL: AY061910; AAL31237.1; -;
 KW Ribosomal protein; Multigene family.
 FT CONFLICT 17 19 QTP -> RHQ (IN REF. 1).
 SQ SEQUENCE 62 AA: 6887 MW: 9508F3EB72F53F33 CRC64;
 Query Match 37.3%; Score 22; DB 1; Length 62;
 Best Local Similarity 100.0%; Pred. No. 9.7e-16;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVHGLARAGKVRGQTPKVAQ 22
 ID 1 KVVHGLARAGKVRGQTPKVAQ 24
 DB 3 KVHGLARAGKVRGQTPKVAQ 24
 RESULT 3
 RS30_ORYLA STANDARD: PRT; 59 AA.
 AC Q9M6Y0;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S30.
 GN FAU OR RPS30.
 OS Oryzias latipes (Medaka fish) (Japanese ricefish)
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;
 CC Acanthopterygii; Acanthopterygii; Percomorpha; Atherinomorpha;
 CC Belontiiformes; Adrianichthyidae; Oryziinae; Oryzias.
 OC NCBI_TaxID=8090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20070552; PubMed=10603084;
 RA Henrich T., Witbrodt J.;
 RT "An in situ hybridization screen for the rapid isolation of
 RT differentially expressed genes.";
 RL Dev. Genes Evol. 210:28-33(2000).
 CC -1- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A
 CC C-TERMINAL EXTENSION PROTEIN (CEP) OF A UBIQUITIN-LIKE PROTEIN.
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL: AJ238274; CAB40969.1; ALT_INIT.
 KW Ribosomal protein.
 SQ SEQUENCE 59 AA: 6660 MW: E91B9C088C7772CF CRC64;
 Query Match 30.5%; Score 18; DB 1; Length 59;
 Best Local Similarity 100.0%; Pred. No. 1.1e-11;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 37 QYNRRFVNVVPTFGKKG 54
 ID 37 QYNRRFVNVVPTFGKKG 54
 DB 37 QYNRRFVNVVPTFGKKG 54
 RESULT 4
 RS30_PLAFA STANDARD: PRT; 58 AA.
 AC Q96269;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 30-MAY-2000 (Rel. 39, Last annotation update)
 DE 40S ribosomal protein S30.
 GN RPS30 OR PFB0885W.
 OS Plasmodium falciparum.
 CC Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
 OC NCBI_TaxID=5833;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99021743; PubMed=9804551;
 RA Gardner M.J., Tettelin H., Carnucci D.J., Cummings L.M., Aravind L.,
 RA Koonin E.V., Shalton S., Mason T., Yu K., Fujii C., Pederson J.,
 RA Shen K., Jing J., Aston C., Lai Z., Schwartz D.C., Pertea M.,
 RA Salzberg S., Zhou L., Sutton G.G., Clayton R., White O., Smith H.O.,
 RA Fraser C.M., Adams M.D., Venter J.C., Hoffman S.L.;
 RT "Chromosome 2 sequence of the human malaria parasite Plasmodium
 RT falciparum.";
 RL Science 282:1126-1132(1998).
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
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 CC -----
 DR EMBL: AE001422; AAC71966.1; -;
 KW Ribosomal protein.
 SQ SEQUENCE 58 AA: 6488 MW: 525675AE74D04F5F CRC64;
 Query Match 20.3%; Score 12; DB 1; Length 58;
 Best Local Similarity 100.0%; Pred. No. 1.4e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 KVHGLARAGK 12
 ID 1 KVVHGLARAGK 14
 DB 3 KVHGLARAGK 14
 RESULT 5
 RS30_SCHPO STANDARD: PRT; 61 AA.
 AC Q42952; O14314;
 DT 15-DEC-1998 (Rel. 37, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE 40S ribosomal protein S30.
 GN (RPS30A OR RPS30 OR SPAC19B12.04) OR (RPS30B OR SPBC19G7.03C).
 OS Schizosaccharomyces pombe (Fission yeast).
 CC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
 CC Schizosaccharomycetaceae; Schizosaccharomycetaceae;

OC Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 OX NCBI_TaxID=8022;
 RN [1]
 RP SEQUENCE, FUNCTION, AND MASS SPECTROMETRY.
 RC TISSUE=Skin mucus;
 RA Fernandes J.M.O., Smith V.J.;
 RT "A novel antimicrobial function for a ribosomal peptide from skin
 secretions of rainbow trout."
 RL Submitted (APR-2002) to the SWISS-PROT data bank.
 CC -1- FUNCTION: Has antibacterial activity against Gram-positive
 bacteria.
 CC -1- MASS SPECTROMETRY: MW=6676.6; METHOD=MALDI.
 CC -1- SIMILARITY: BELONGS TO THE S30E FAMILY OF RIBOSOMAL PROTEINS.
 KW Ribosomal protein; Antibiotic.
 FT NON_TER 11
 SQ SEQUENCE 11 AA; 1123 MW; 2312AB630DD735B8 CRC64;
 Query Match 18.6%; Score 11; DB 1; Length 11;
 Best Local Similarity 100.0%; Pred. No. 3.4e-05;
 Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 KVGSLARAGK 11
 Db [1]
 1 KVGSLARAGK 11
 RESULT 8
 HNS_PROVU STANDARD; PRT; 133 AA.
 AC P18818;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-NOV-1995 (Rel. 32, Last annotation update)
 DE DNA-binding protein H-NS (Histone-like protein HLP-II).
 GN HNS OR HNSA.
 OS Proteus vulgaris.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Proteus.
 OX NCBI_TaxID=585;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89171270; PubMed=2494066;
 RA Teana A., Falconi M., Scariato V., Lammi M., Pon C.L.;
 RT "Characterization of the structural genes for the DNA-binding protein
 H-NS in Enterobacteriaceae."
 RL FEBS Lett. 244:34-38(1989).
 CC -1- FUNCTION: H-NS BINDS TIGHTLY TO DS-DNA, INCREASES ITS THERMAL
 STABILITY AND INHIBITS TRANSCRIPTION. IT ALSO BINDS TO SS-DNA AND
 RNA BUT WITH A MUCH LOWER AFFINITY. H-NS HAS POSSIBLE HISTONE-LIKE
 FUNCTION. MAY BE A GLOBAL TRANSCRIPTIONAL REGULATOR THROUGH ITS
 ABILITY TO BIND TO CURVED DNA SEQUENCES, WHICH ARE FOUND IN
 REGIONS UPSTREAM OF A CERTAIN SUBSET OF PROMOTERS. IT PLAYS A ROLE
 IN THE THERMAL CONTROL OF PILI PRODUCTION. IT IS SUBJECT TO THE
 TRANSCRIPTIONAL AUTO-REPRESSION. IT BINDS PREFERENTIALLY TO THE
 UPSTREAM REGION OF ITS OWN GENE RECOGNIZING TWO SEGMENTS OF DNA ON
 BOTH SIDES OF A BEND CENTERED AROUND -150 (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE HISTONE-LIKE PROTEIN H-NS FAMILY.
 DR PIR: S02776; S02776.
 DR HSP: P08936; 1HNR.
 DR InterPro: IPR001801; Histone_HNS.
 DR Pfam: PF00816; Histone_HNS; 1.
 DR ProDom: PD007337; Histone_HNS; 1.
 DR SMART: SM00528; HNS; 1.
 KW DNA-binding; Transcription regulation; Repressor.
 FT INT_MET 0
 SQ SEQUENCE 133 AA; 15134 MW; B92C49F7995C5ED5 CRC64;
 Query Match 11.9%; Score 7; DB 1; Length 133;
 Best Local Similarity 100.0%; Pred. No. 3.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 28 KTGRAKR 34

Db 82 KTGRAKR 88
 [1]
 RESULT 9
 YOC2_CAEEL STANDARD; PRT; 346 AA.
 ID YOC2_CAEEL
 AC Q09261;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 01-NOV-1997 (Rel. 35, Last annotation update)
 DE Hypothetical 39.2 kDa protein C32A3.2 in chromosome III.
 GN C32A3.2.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2;
 RA Thomas K.;
 RL Submitted (FEB-1995) to the EMBL/GenBank/DBJ databases.
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 or send an email to license@isb-sib.ch).
 CC EMBL; 248241; CAA88285.1; -
 DR WormPep: C32A3.2; CE01506.
 DR Hypothetical protein.
 KW Hypothetical protein.
 SQ SEQUENCE 346 AA; 39221 MW; D511225F5062B420 CRC64;
 Query Match 11.9%; Score 7; DB 1; Length 346;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 23 EKKKKK 29
 Db [1]
 6 EKKKKK 12
 RESULT 10
 COLB_HUMAN STANDARD; PRT; 489 AA.
 ID COLB_HUMAN
 AC Q9BR76;
 DT 15-JUN-2002 (Rel. 41, Created)
 DT 15-JUN-2002 (Rel. 41, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Coronin 1B (Coronin 2).
 GN CORO1B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Placenta;
 RA Strausberg R.;
 RL Submitted (APR-2001) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY BE INVOLVED IN CYTOKINESIS, MOTILITY, AND SIGNAL
 TRANSDUCTION (BY SIMILARITY).
 CC -1- SUBUNIT: BINDS ACTIN (BY SIMILARITY).
 CC -1- SIMILARITY: CONTAINS 5 WD REPEATS (TRP-ASP DOMAINS).
 CC -1- SIMILARITY: BELONGS TO THE CORONIN FAMILY OF WD-REPEAT PROTEINS.
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DR EMBL; BC006449; AA064449.1; -;
 DR Genew; HGNC:2253; CORO1B.
 DR InterPro; IPR001680; WD40.
 DR Pfam; PF00400; WD40; 3.
 DR ProDom; PD000018; WD40; 1.
 DR SMART; SM00320; WD40; 3.
 DR PROSITE; PS00678; WD_REPEATS_1; 1.
 DR PROSITE; PS00082; WD_REPEATS_2; 2.
 DR PROSITE; PS0294; WD_REPEATS_REGION; 1.
 KW Actin-binding; Repeat; WD repeat; Coiled coil.
 FT REPEAT 80 120 WD 1.
 FT REPEAT 130 170 WD 2.
 FT REPEAT 174 213 WD 3.
 FT REPEAT 217 260 WD 4.
 FT REPEAT 265 305 WD 5.
 FT DOMAIN 449 474 COILED COIL (POTENTIAL).
 SQ SEQUENCE 489 AA; 54234 MW; A6012FDA683ECB59 CRC64;

Query Match 11.9%; Score 7; DB 1; Length 489;
 Best Local Similarity 100.0%; Pred. No. 10;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 4 GSLARAG 10

|||||

Db 442 GSLARAG 448

RESULT 11

POLS_EEVVM
 ID POLS_EEVVM STANDARD; PRT; 1254 AA.
 AC P36331; Q66587; Q66588; Q66589; Q66590; Q66591;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Structural polyprotein (p130) [Contains: Coat protein C (EC 3.4.21.-) (Capsid protein C); Spike glycoprotein E3; Spike glycoprotein E2; 6 kDa peptide; Spike glycoprotein E1].
 DE Venezuelan equine encephalitis virus (strain Mena II).
 OS Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
 OC Alphavirus.
 OX NCBI_TaxID=36384;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=93187617; PubMed=8445371;
 RA Snider J.M., Kinney R.M., Tsuchiya K.R., Trent D.W.;
 RT "Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB viruses are not evolutionary derivatives of enzootic VEE subtype I-E or II viruses."
 RT J. Gen. Virol. 74:519-523 (1993).
 RL
 CC -!- FUNCTION: THE CAPSID PROTEIN IS AN AUTO-PROTEASE.
 CC -!- PTM: SPECIFIC ENZYMIC CLEAVAGES IN VIVO YIELD MATURE PROTEINS.
 CC -!- MISCELLANEOUS: THE 6 kDa POLYPEPTIDE PROBABLY SERVES AS THE SIGNAL SEQUENCE FOR THE MEMBRANE GLYCOPROTEIN E1, WHICH IS THE VIRAL HEMAGGLUTININ.
 CC -!- SIMILARITY: THE PROTEASE BELONGS TO PEPTIDASE FAMILY S3.

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DR EMBL; L04599; AAA42990.1; -;
 DR EMBL; L04599; AAA42989.1; ALT_TERM.
 DR EMBL; L04599; AAA42991.1; ALT_SEQ.
 DR EMBL; L04599; AAA42992.1; ALT_SEQ.
 DR EMBL; L04599; AAA42993.1; ALT_SEQ.

DR EMBL; L04599; AAA42994.1; ALT_INIT.
 DR PIR; JQ1979; JQ1979.
 DR HSSP; P03315; IVCP.
 DR MEROPS; S03.001; -;
 DR InterPro; IPR002548; Alpha_E1_glycop.
 DR InterPro; IPR000936; Alpha_E2_glycop.
 DR InterPro; IPR002533; Alpha_E3_glycop.
 DR InterPro; IPR001836; Alpha_core.
 DR InterPro; IPR000930; Togavirin.
 DR Pfam; PF00943; Alpha_E2_glycop; 1.
 DR Pfam; PF00944; Alpha_core; 1.
 DR Pfam; PF01563; Alpha_E3_glycop; 1.
 DR Pfam; PF01589; Alpha_E1_glycop; 1.
 DR PRINTS; PR00798; TOGAVIRIN.
 KW Coat protein; Polyprotein; Transmembrane; Glycoprotein; Hydrolase;
 KW Serine protease.
 FT CHAIN 1 274 COAT PROTEIN C.
 FT CHAIN 275 333 SPIKE GLYCOPROTEIN E3.
 FT CHAIN 334 756 SPIKE GLYCOPROTEIN E2.
 FT CHAIN 757 812 6 KDA PEPTIDE.
 FT CHAIN 813 1254 SPIKE GLYCOPROTEIN E1.
 FT ACT_SITE 151 151 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 157 157 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT ACT_SITE 225 225 CHARGE RELAY SYSTEM (BY SIMILARITY).
 FT TRANSMEM 701 721 POTENTIAL.
 FT TRANSMEM 794 813 POTENTIAL.
 FT TRANSMEM 1231 1248 POTENTIAL.
 FT CARBOHYD 47 47 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 285 285 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 545 545 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 651 651 N-LINKED (GLCNAC. . .) (POTENTIAL).
 FT CARBOHYD 946 946 N-LINKED (GLCNAC. . .) (POTENTIAL).
 SQ SEQUENCE 1254 AA; 138343 MW; FB9DE8265F20211 CRC64;
 Query Match 11.9%; Score 7; DB 1; Length 1254;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30

|||||

Db 88 KKKKKTG 94

RESULT 12

R27A_DICDI
 ID R27A_DICDI STANDARD; PRT; 78 AA.
 AC P14797;
 DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 01-FEB-1996 (Rel. 33, Last annotation update)
 DE 40S ribosomal protein S27a.
 OS Dictyostellium discoideum (Slime mold).
 OC Eukaryota; Mycetozoa; Dictyosteliida; Dictyostellium.
 OX NCBI_TaxID=44889;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=89352609; PubMed=2548604;
 RA Ohmachi T., Giorda R., Shaw D.R., Ennis H.L.;
 RT "Molecular organization of developmentally regulated Dictyostellium discoideum ubiquitin cDNAs".
 RL Biochemistry 28:5226-5231 (1989).
 CC -!- MISCELLANEOUS: THIS RIBOSOMAL PROTEIN IS SYNTHESIZED AS A C-TERMINAL EXTENSION PROTEIN (CEP) OF UBIQUITIN.
 CC -!- SIMILARITY: BELONGS TO THE S27AE FAMILY OF RIBOSOMAL PROTEINS.
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DR EMBL; M23750: AAA33264.1; ALT_INIT.
DR PIR; E34080: UQDOR7.
DR DictyDb; DD01026: -.
DR InterPro; IPR002906; Ribosomal_S27.
DR Pfam; PF01599; Ribosomal_S27; 1.
KW Ribosomal protein; Zinc-finger; Metal-binding.
FT DOMAIN 1 24 LYS-RICH (HIGHLY BASIC).
FT ZN_FING 46 69 C4-TYPE.
SQ SEQUENCE 78 AA; 8915 MW; F77B3E09D1B7246F CRC64;

Query Match 10.2%; Score 6; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
DB 4 KKKKKT 9

RESULT 13
RS18_BACSU
ID RS18_BACSU STANDARD; PRT; 78 AA.
AC P21475;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE 30S ribosomal protein S18 (BS21).
OS RPSR.
GN Bacillus subtilis.
OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
OX NCBI_TaxID=1423;
RN 1;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=96051395; PubMed=7584024;
RA Ogawara N., Nakai S., Yoshikawa H.;
RA "Systematic sequencing of the 180 kilobase region of the Bacillus
RT subtilis chromosome containing the replication origin.";
RL DNA Res. 1:1-14(1994).
RN 12;
RP SEQUENCE FROM N.A.
RC STRAIN=168;
RX MEDLINE=98044033; PubMed=9384377;
RA Kunst F., Ogawara N., Moszer I., Albertini A.M., Alloni G.,
RA Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S.,
RA Borriess R., Boursier L., Brans A., Braun M., Brignell S.C., Bron S.,
RA Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M.,
RA Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A.,
RA Denizot F., Devine K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T.,
RA Entian K.D., Errington J., Fabret C., Ferrari E., Foulger D.,
RA Fritz C., Fujita M., Fujita Y., Fuma S., Galizzi A., Galleron N.,
RA Ghim S.Y., Glaser P., Goffeau A., Gollightly E.J., Grandi G.,
RA Guiseppi G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A.,
RA Hilbert H., Holsappel S., Hosono S., Hulio M.F., Itaya M., Jones L.,
RA Joris B., Karamata D., Kasahara Y., Klaerr-Blanchard M., Klein C.,
RA Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M.,
RA Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V.,
RA Lee S.M., Levine A., Liu H., Masuda S., Mauel C., Medigue C.,
RA Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M.,
RA Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H.,
RA Parro V., Pohl T.M., Portetelle D., Porwollik S., Prescott A.M.,
RA Presecan E., Pujic P., Purnelle B., Rapoport G., Rey M., Reynolds S.,
RA Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadaie Y.,
RA Sato T., Scanlan E., Schleich S., Schroeter R., Scoffone F.,
RA Sekiguchi J., Sekowska A., Seror S.J., Serro P., Shin B.S., Soldo B.,
RA Sorokin A., Taccini E., Takagi T., Takahashi H., Takemaru K.,
RA Takeuchi M., Tamakoshi A., Tanaka T., Terpstra P., Tognoni A.,
RA Tosato V., Uchiyama S., Vandenbol M., Vannier F., Vassarotti A.,
RA Viari A., Wambutt R., Wedler E., Wedler H., Weitzenecker T.,
RA Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K.,
RA Yoshida K., Yoshikawa H.F., Zumstein E., Yoshikawa H., Danchin A.;
RT "The complete genome sequence of the Gram-positive bacterium Bacillus
RT subtilis.";

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RL Nature 390:249-256(1997).
RN [3]
RP SEQUENCE OF 1-23.
RX MEDLINE=82219212; PubMed=6806564;
RT Higo K.I., Otake E., Osawa S.;
RT "Purification and characterization of 30S ribosomal proteins from
RT Bacillus subtilis: correlation to Escherichia coli 30S proteins.";
RL Mol. Gen. Genet. 185:239-244(1982).
CC 1- FUNCTION: This protein has been implicated in aminoacyl-transfer
CC RNA binding. It appears to be situated at the decoding site of
CC messenger RNA.
CC 1- SIMILARITY: BELONGS TO THE S18P FAMILY OF RIBOSOMAL PROTEINS.
CC
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CC
CC EMBL; D26185; BAA05219.1; ALT_INIT.
CC EMBL; Z99124; CAB16126.1; ALT_INIT.
CC PIR; S11368; S11368.
CC Subtilist; BG10047; rpsr.
CC InterPro; IPR001648; Ribosomal_S18.
CC Pfam; PF01084; Ribosomal_S18; 1.
CC PRINTS; PR00974; RIBOSOMALS18.
CC ProDom; PD002239; Ribosomal_S18; 1.
CC TIGRFAMS; TIGR00165; S18; 1.
CC PROSITE; PS00057; RIBOSOMAL_S18; 1.
CC KW Ribosomal protein; RNA-binding; Complete proteome.
CC FT INIT MET 0
CC SEQUENCE 78 AA; 8838 MW; 1CF19CE039C64FF2 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 78;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 30 GRAKRR 35
DB 7 GRAKRR 12

RESULT 14
EX7S_VIBCH
ID EX7S_VIBCH STANDARD; PRT; 80 AA.
AC Q9KTL1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Probable exodeoxyribonuclease VII small subunit (EC 3.1.11.6)
DE (Exonuclease VII small subunit).
GN XSEB OR VC0891.
OS Vibrio cholerae.
OC Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
OX NCBI_TaxID=666;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=El Tor N16961 / Serotype O1;
RX MEDLINE=20406833; PubMed=10952301;
RA Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
RA Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A.,
RA Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D.,
RA Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P.,
RA McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O.,
RA Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
RA Fraser C.M.;
RT "DNA sequence of both chromosomes of the cholera pathogen Vibrio
RT cholerae.";
RL Nature 406:477-483(2000).
CC 1- FUNCTION: BIDIRECTIONALLY DEGRADABLE SINGLE-STRANDED DNA INTO LARGE
CC ACID-INSOLUBLE OLIGONUCLEOTIDES, WHICH ARE THEN DEGRADED FURTHER

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```
CC INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
CC -|- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -|- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
CC SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE XSEB FAMILY.
CC -----
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CC -----
DR EMBL: AE004173; AAF94053.1; -.
DR TIGR: VC0891; -.
DR InterPro: IPR003761; Exonuc_VII_S.
DR Pfam: PF02609; Exonuc_VII_S; 1.
DR TIGRFAMs: TIGR01280; xseB; 1.
KW Hydrolase; Nuclease; Exonuclease; Complete proteome.
SQ SEQUENCE 80 AA; 9911 MW; F9B7F5A9C6821DD1 CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 80;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 44 SLARAG 49
-----
RESULT 15
YGRM_MICEC
ID YGRM_MICEC STANDARD; PRT; 105 AA.
AC P24620;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-MAR-1992 (Rel. 21, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in grm 3' region (Fragment).
OS Micromonospora echinospora (Micromonospora purpurea).
CC Bacteria; Actinobacteria; Actinobacteridae (class); Actinobacteridae;
CC Actinomycetales; Micromonosporineae; Micromonosporaceae;
CC Micromonospora.
CC NCBI_TaxID=1877;
CC [1]
CC SEQUENCE FROM N.A.
RX MEDLINE=91192615; PubMed=2013410;
RA Kelemen G.H., Cundliffe E., Financsek I.;
RT "Cloning and characterization of gentamicin-resistance genes from
RT Micromonospora purpurea and Micromonospora rosea.";
RL Gene 98:53-60(1991).
-----
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CC -----
DR EMBL: M55520; AAA25337.1; -.
DR PIR: PW0017; PW0018.
KW Antibiotic resistance; Hypothetical protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11111 MW; 0B398039381DB012 CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 44 SLARAG 49
-----
CC INTO SMALL ACID-SOLUBLE OLIGONUCLEOTIDES (BY SIMILARITY).
CC -|- CATALYTIC ACTIVITY: Exonucleolytic cleavage in either 5'- to 3'-
CC or 3'- to 5'-direction to yield nucleoside 5'-phosphates.
CC -|- SUBUNIT: HETEROOLIGOMER COMPOSED OF LARGE AND SMALL SUBUNITS (BY
CC SIMILARITY).
CC -|- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC -|- SIMILARITY: BELONGS TO THE XSEB FAMILY.
CC -----
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CC -----
DR EMBL: M55520; AAA25337.1; -.
DR PIR: PW0017; PW0018.
KW Antibiotic resistance; Hypothetical protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11111 MW; 0B398039381DB012 CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 44 SLARAG 49
-----
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Db 11 SLARAG 16
-----
RESULT 16
YGRM_MICRO
ID YGRM_MICRO STANDARD; PRT; 105 AA.
AC P24621;
DT 01-MAR-1992 (Rel. 21, Created)
DT 01-FEB-1996 (Rel. 33, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Hypothetical protein in grm 3' region (Fragment).
OS Micromonospora rosea.
CC Bacteria; Actinobacteria; Actinobacteridae (class); Actinobacteridae;
CC Actinomycetales; Micromonosporineae; Micromonosporaceae;
CC Micromonospora.
CC NCBI_TaxID=1878;
CC [1]
CC SEQUENCE FROM N.A.
RX MEDLINE=91192615; PubMed=2013410;
RA Kelemen G.H., Cundliffe E., Financsek I.;
RT "Cloning and characterization of gentamicin-resistance genes from
RT Micromonospora purpurea and Micromonospora rosea.";
RL Gene 98:53-60(1991).
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CC -----
DR EMBL: M55521; AAA25339.1; -.
DR PIR: PW0018; PW0018.
KW Antibiotic resistance; Hypothetical protein.
FT NON_TER 105 105
SQ SEQUENCE 105 AA; 11112 MW; 56125793440BA48C CRC64;
-----
Query Match 10.2%; Score 6; DB 1; Length 105;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 5 SLARAG 10
DB 11 SLARAG 16
-----
RESULT 17
RL19_TREPA
ID RL19_TREPA STANDARD; PRT; 123 AA.
AC O83879;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DE 50S ribosomal protein L19.
GN RPLS OR rp0909.
OS Treponema pallidum.
CC Bacteria; Spirochaetales; Spirochaetaceae; Treponema.
CC NCBI_TaxID=160;
CC [1]
CC SEQUENCE FROM N.A.
RX STRAIN=Nichols;
RC MEDLINE=98332770; PubMed=9665876;
RA Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G.,
RA Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A.,
RA Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J.,
RA Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T.,
RA McDonald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S.,
RA Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
RA Venter J.C.;
RT "Complete genome sequence of Treponema pallidum, the syphilis
RT spirochete.";
```

RL Science 281:375-388(1998).
 CC -1- FUNCTION: THIS PROTEIN IS LOCATED AT THE 30S-50S RIBOSOMAL SUBUNIT
 CC INTERFACE AND MAY PLAY A ROLE IN THE STRUCTURE AND FUNCTION OF THE
 CC AMINOACYL-TRNA BINDING SITE (BY SIMILARITY).
 CC -1- SIMILARITY: BELONGS TO THE L19P FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL; AE001259; AAC65861.1; -
 CC InterPro: TP0909; -
 CC InterPro: IPR001857; Ribosomal_L19.
 CC Pfam; PF01245; Ribosomal_L19; 1.
 CC PRINTS; PR00061; Ribosomal_L19.
 CC ProDom; PD002979; Ribosomal_L19; 1.
 CC TIGRFAMs; TIGR01024; rPLS.bact; 1.
 CC PROSITE; PS01015; RIBOSOMAL_L19; 1.
 CC Ribosomal protein; Complete proteome.
 CC KW RIBOSOMAL_L19; 1.
 CC SEQUENCE 123 AA; 14192 MW; 123E652CB4B545EF CRC64;
 CC -----
 CC Query Match 10.2%; Score 6; DB 1; Length 123;
 CC Best Local Similarity 100.0%; Pred. No. 32;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 8 RAGKVR 13
 CC DB 89 RAGKVR 94
 CC | | | | |
 CC -----
 CC RESULT 18
 CC RS25_HUMAN STANDARD; PRT; 125 AA.
 CC AC P25111;
 CC DT 01-MAY-1992 (Rel. 22, Created)
 CC DT 01-MAY-1992 (Rel. 22, Last sequence update)
 CC DT 15-JUN-2002 (Rel. 41, Last annotation update)
 CC DE 40S ribosomal protein S25.
 CC GN RPS25.
 CC OS Homo sapiens (Human),
 CC OS Mus musculus (Mouse), and
 CC OS Rattus norvegicus (Rat).
 CC OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 CC OX NCBI_TaxID=9606, 10090, 10116;
 CC RN [1]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Human;
 CC RA MEDLINE=92084127; PubMed=1748303;
 CC LI M., Latoud C., Center M.S.;
 CC RT "Cloning and sequencing a cDNA encoding human ribosomal protein S25";
 CC Gene 107:329-333(1991).
 CC RN [2]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Human;
 CC RA MEDLINE=21864036; PubMed=11875025;
 CC Yoshihama M., Uechi T., Asakawa S., Kawasaki K., Kato S., Higa S.,
 CC Maeda N., Minoshima S., Tanaka T., Shimizu N., Kenmochi N.;
 CC RT "The human ribosomal protein genes: sequencing and comparative
 CC analysis of 73 genes";
 CC RL Genome Res. 12:379-390(2002).
 CC RN [3]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Human;
 CC RA Strausberg R.;
 CC Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 CC RN [4]
 CC RP SEQUENCE FROM N.A.
 CC RC SPECIES=Mouse; STRAIN=C57BL/6J;
 CC -----

RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Arakawa T., Harai A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
 RA Alizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
 RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Sakimi L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsch G.,
 RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
 RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
 RA Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
 RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
 RA Hayashizaki Y.;
 RA "Functional annotation of a full-length mouse cDNA collection";
 RN Nature 409:685-690(2001).
 RN [5]
 RN SEQUENCE FROM N.A.
 RP SPECIES=Mouse; TISSUE=Breast tumor;
 RA Strausberg R.;
 RN Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RN SEQUENCE FROM N.A.
 RC SPECIES=Rat; STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=92378645; PubMed=1354961;
 RA Chan Y.-L., Wool I.G.;
 RT "The primary structure of rat ribosomal protein S25";
 RL Biochem. Biophys. Res. Commun. 186:1688-1693(1992).
 CC -1- SIMILARITY: BELONGS TO THE S25E FAMILY OF RIBOSOMAL PROTEINS.
 CC -----
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 CC -----
 CC EMBL; M64716; AAA16105.1; -
 CC EMBL; AB061844; BAB79482.1; -
 CC EMBL; BC003537; AAH03537.1; -
 CC EMBL; BC004294; AAH04294.1; -
 CC EMBL; BC004986; AAH04986.1; -
 CC EMBL; AK012696; BAB28417.1; -
 CC EMBL; BC002088; AAH02088.1; -
 CC EMBL; X62482; CAA44349.1; -
 CC PIR; S17353; R3RT25.
 CC PIR; JH0691; JH0691.
 CC PIR; JQ1347; JQ1347.
 CC Genew; HGNC:10413; RPS25.
 CC MIM; 180465; -
 CC MGD; MGI:1922867; Rps25.
 CC InterPro: IPR004977; Ribosomal_S25.
 CC Pfam; PF03297; Ribosomal_S25; 1.
 CC KW Ribosomal protein.
 CC SEQUENCE 125 AA; 13742 MW; B8E05F04FC2F1A9 CRC64;
 CC -----
 CC Query Match 10.2%; Score 6; DB 1; Length 125;
 CC Best Local Similarity 100.0%; Pred. No. 33;
 CC Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 CC -----
 CC QY 4 GSLARA 9
 CC DB 81 GSLARA 86
 CC | | | | |
 CC -----
 CC RESULT 19
 CC RS11_RICPR

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CC -----
DR EMBL: U231147; AAC46687.1; -
DR Wormpep; C18H9.2; CE01802.
DR Hypothetical protein.
KW
SQ SEQUENCE 128 AA; 13666 MW; C7A64D960B95E2EC CRC64;

Query Match 10.2%; Score 6; DB 1; Length 128;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 KKKKK 29
 |||||
Db 84 KKKKK 89

RESULT 21
YNO3_YEAST
ID YNO3_YEAST STANDARD; PRT; 130 AA.
AC P53908;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE Hypothetical 15.3 kDa protein in MFA2-MEP2 intergenic region.
GN YNL143C OR N1206 OR N1795.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RS SEQUENCE FROM N.A.
RP STRAIN=S288C;
RC MEDLINE=96109932; PubMed=8619318;
RA Mallet L., Bussereau F., Jaquet M.;
RT "A 43.5 kb segment of yeast chromosome XIV, which contains MFA2,
RT MEP2, CAP/SRV2, NAM9, FKB1/FPRI/RBP1, MOM22 and CPT1, predicts an
RT adenosine deaminase gene and 14 new open reading frames.";
RL Yeast 11:1195-1209(1995).
RS
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CC -----
DR EMBL: Z46843; CAA86883.1; -
DR EMBL: Z714119; CAA96026.1; -
DR SGD; S0005087; YNL143C.
KW Hypothetical protein.
SQ SEQUENCE 130 AA; 15319 MW; 29070E47FC63436D CRC64;

Query Match 10.2%; Score 6; DB 1; Length 130;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKK 28
 |||||
Db 48 EKKKK 53

RESULT 22
YKDI_YEAST
ID YKDI_YEAST STANDARD; PRT; 137 AA.
AC P36098;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 01-NOV-1995 (Rel. 32, Last annotation update)
DE Hypothetical 15.6 kDa protein in IXRI-TFAL intergenic region.

GN YKL031W OR YKL244.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=94262309; PubMed=8203146;
RA Purnelle B., Skala J., van Dyck L., Goffeau A.;
RT "Analysis of an 11.7 kb DNA fragment of chromosome XI reveals a new
RT tRNA gene and four new open reading frames including a leucine zipper
RL protein and a homologue to the yeast mitochondrial regulator ABF2.";
RN Yeast 10:125-130(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Rieger M.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC -----
DR EMBL: X71622; NOT_ANNOTATED_CDS.
DR EMBL: Z28031; CAA81866.1; -.
DR PIR: S37848; S37848.
DR SGD: S0001514; YKL031W.
KW Hypothetical protein; Transmembrane.
FT TRANSMEM 36 52 POTENTIAL.
FT TRANSMEM 113 129 POTENTIAL.
SQ SEQUENCE 137 AA; 15626 MW; 82908E55C7E37CFC CRC64;

Query Match 10.2%; Score 6; DB 1; Length 137;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
DB 60 EKKKKK 65

RESULT 23
RS16_CANAL STANDARD; PRT; 142 AA.
AC 094017;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 40S ribosomal protein S16.
GN RPS16 OR CA49C10.01C.
OC Candida albicans (Yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX Saccharomycetales; Mitosporic Saccharomycetales; Candida.
NCBI_TaxID=5476;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1161;
RA Taylor K., Harris D., Barrell B.G., Rajandream M.A.;
RL Submitted (NOV-1998) to the EMBL/GenBank/DBJ databases.
CC -!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
CC -----
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CC -----

DR EMBL: AL033497; CAA21965.1; -.
DR InterPro: IPR000754; Ribosomal_S9.
DR Pfam: PF00380; Ribosomal_S9; 1.
DR ProDom: PD001627; Ribosomal_S9; 1.
DR PROSITE: PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein.
SQ SEQUENCE 142 AA; 15739 MW; 19408A7791FF4356 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKKK 53
DB 8 TFGKKK 13

RESULT 24
RS16_YEAST STANDARD; PRT; 142 AA.
AC P40213; P26787;
DT 01-AUG-1992 (Rel. 23, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE 40S ribosomal protein S16 (RP61R).
GN (RPS16A OR RP61R OR YMR143W OR YMR9375.12) AND (RPS16B OR YDL083C).
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OX Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A. (RPS16A).
RC STRAIN=S288C / AB972;
RA Badcock K., Churcher C., Barrell B.G., Rajandream M.A., Walsh S.V.;
RL Submitted (DEC-1994) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A. (RPS16B).
RA Wambutt R., Wedler H., Wedler E., Scharfe M.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP PRELIMINARY PARTIAL SEQUENCE OF 1-25.
RX MEDLINE=92184799; PubMed=1544921;
RA Takakura H., Tsunasawa S., Miyagi M., Warner J.R.;
RT "NH2-terminal acetylation of ribosomal proteins of Saccharomycetes
RT cerevisiae";
RL J. Biol. Chem. 267:5442-5445(1992).
CC -!- MISCELLANEOUS: THERE ARE TWO GENES FOR S16 IN YEAST.
CC -!- SIMILARITY: BELONGS TO THE S9P FAMILY OF RIBOSOMAL PROTEINS.
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CC -----
DR EMBL: Z47071; CAA87357.1; -.
DR EMBL: Z74131; CAA98649.1; -.
DR SGD: S0004751; RPS16A.
DR SGD: S0002241; RPS16B.
DR InterPro: IPR000754; Ribosomal_S9.
DR Pfam: PF00380; Ribosomal_S9; 1.
DR ProDom: PD001627; Ribosomal_S9; 1.
DR PROSITE: PS00360; RIBOSOMAL_S9; 1.
KW Ribosomal protein; Acetylation; Multigene family.
FT INIT_MET 0 0
FT MOD_RES 1 1 ACETYLATION.
SQ SEQUENCE 142 AA; 15716 MW; 15873374B3262144 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 142;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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QY 48 TFGKKK 53
Db 8 TFGKKK 13

RESULT 25
END7_BPT4
ID END7_BPT4 STANDARD; PRT; 157 AA.
AC P13340; Q38426; Q9T0V4;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Recombination endonuclease VII (EC 3.1.1.-) (Protein Gp49).
GN 49.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RX MEDLINE=87203398; PubMed=3575111;
RA Tomaszewski J., Rueger W.;
RT "Nucleotide sequence and primary structures of gene products coded
RT for by the T4 genome between map positions 48,266 kb and 39,166 kb.";
RL Nucleic Acids Res. 15:3632-3633(1987).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE INITIATION.
RX MEDLINE=89065345; PubMed=2374005;
RA Barck K.A., Powell D., Trupin M., Mosig G.;
RT "Regulation of two nested proteins from gene 49 (recombination
RT endonuclease VII) and of a lambda RexA-like protein of bacteriophage
RT T4.";
RL Genetics 120:329-343(1988).
RN [3]
RP SEQUENCE FROM N.A.
RA Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RA Mesyanzhinov V., Rueger W., Stidham T., Thomas E.;
RT "Bacteriophage T4 genome analysis.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CLEAVES DNA CRUCIFORM AND Y-STRUCTURES AS WELL AS
CC HETERODUPLEX LOOPS.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms are produced by alternative
CC initiation.
CC -----
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CC -----
DR EMBL; X12629; CAA311148.1; -
DR EMBL; X12629; CAA311149.1; -
DR EMBL; Y00122; CAA68307.1; -
DR EMBL; AF158101; AAD42477.1; -
DR EMBL; AF158101; AAD42687.1; ALT_INIT.
DR PIR; A30291; ZNBPT9.
DR InterPro; IPR004211; Endonuclease_7.
DR Pfam; PF02945; endonuclease_7; 3.
KW Hydrolase; Endonuclease; Nuclease; Alternative initiation.
FT CHAIN 1 157 RECOMBINATION ENDONUCLEASE VII, LONG
FT ISOFORM.
FT CHAIN 53 157 RECOMBINATION ENDONUCLEASE VII, SHORT
FT ISOFORM.
FT INIT_MET 53 53 FOR SHORT ISOFORM.
SQ SEQUENCE 157 AA; 18144 MW; 86233D2A7FC0F9A8 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-----
QY 48 TFGKKK 53
Db 8 TFGKKK 13

RESULT 25
END7_BPT4
ID END7_BPT4 STANDARD; PRT; 157 AA.
AC P13340; Q38426; Q9T0V4;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-JAN-1990 (Rel. 13, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Recombination endonuclease VII (EC 3.1.1.-) (Protein Gp49).
GN 49.
OS Bacteriophage T4.
OC Viruses; dsDNA viruses, no RNA stage; Caudovirales; Myoviridae;
OC T4-like viruses.
OX NCBI_TaxID=10865;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C;
RX MEDLINE=87203398; PubMed=3575111;
RA Tomaszewski J., Rueger W.;
RT "Nucleotide sequence and primary structures of gene products coded
RT for by the T4 genome between map positions 48,266 kb and 39,166 kb.";
RL Nucleic Acids Res. 15:3632-3633(1987).
RN [2]
RP SEQUENCE FROM N.A., AND ALTERNATIVE INITIATION.
RX MEDLINE=89065345; PubMed=2374005;
RA Barck K.A., Powell D., Trupin M., Mosig G.;
RT "Regulation of two nested proteins from gene 49 (recombination
RT endonuclease VII) and of a lambda RexA-like protein of bacteriophage
RT T4.";
RL Genetics 120:329-343(1988).
RN [3]
RP SEQUENCE FROM N.A.
RA Kutter E., Arisaka F., Kunisawa T., Tsugita A., Mosig G.,
RA Mesyanzhinov V., Rueger W., Stidham T., Thomas E.;
RT "Bacteriophage T4 genome analysis.";
RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: CLEAVES DNA CRUCIFORM AND Y-STRUCTURES AS WELL AS
CC HETERODUPLEX LOOPS.
CC -!- ALTERNATIVE PRODUCTS: 2 isoforms are produced by alternative
CC initiation.
CC -----
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CC -----
DR EMBL; X12629; CAA311148.1; -
DR EMBL; X12629; CAA311149.1; -
DR EMBL; Y00122; CAA68307.1; -
DR EMBL; AF158101; AAD42477.1; -
DR EMBL; AF158101; AAD42687.1; ALT_INIT.
DR PIR; A30291; ZNBPT9.
DR InterPro; IPR004211; Endonuclease_7.
DR Pfam; PF02945; endonuclease_7; 3.
KW Hydrolase; Endonuclease; Nuclease; Alternative initiation.
FT CHAIN 1 157 RECOMBINATION ENDONUCLEASE VII, LONG
FT ISOFORM.
FT CHAIN 53 157 RECOMBINATION ENDONUCLEASE VII, SHORT
FT ISOFORM.
FT INIT_MET 53 53 FOR SHORT ISOFORM.
SQ SEQUENCE 157 AA; 18144 MW; 86233D2A7FC0F9A8 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 157;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

-----
QY 9 AGKVRG 14
Db 50 AGKVRG 55

RESULT 26
YK20_YEAST
ID YK20_YEAST STANDARD; PRT; 167 AA.
AC P36133;
DT 01-JUN-1994 (Rel. 29, Created)
DT 01-JUN-1994 (Rel. 29, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE Hypothetical 19.2 kDa protein in GAP1-NAP1 intergenic region.
GN YKR040C.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
OX NCBI_TaxID=4932;
RN [1]
RP SEQUENCE FROM N.A.
RA Urrestarazu L.A., Jauniaux J.-C.;
RL Submitted (MAR-1994) to the EMBL/GenBank/DBJ databases.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z28265; CAA82114.1; -
DR EMBL; Z28266; CAA82117.1; -
DR PIR; S38112; S38112.
DR SGD; S0001748; YKR040C.
KW Hypothetical protein.
FT DOMAIN 144 167 LYS-RICH (HIGHLY BASIC).
SQ SEQUENCE 167 AA; 19222 MW; 51BC98B657A720C2 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 42;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 23 EKKKKK 28
Db 143 EKKKKK 148

RESULT 27
RL14_LEIDO
ID RL14_LEIDO STANDARD; PRT; 175 AA.
AC Q25278;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE Probable 40S ribosomal protein L14 (23 kDa cell surface protein)
DE (LDP 23).
GN RPL14 OR LDP23.
OS Leishmania donovani.
OC Eukaryota; Euklenozoa; Kinetoplastida; Trypanosomatidae; Leishmania.
OX NCBI_TaxID=5661;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LS;
RX MEDLINE=96042140; PubMed=7595213;
RA Campos-Neto A., Soong L., Cordova J.L., Sant'Angelo D., Skeiky Y.A.W.,
RA Rudde N.H., Reed S.G., Janeway C. Jr., McMahon-Pratt D.;
RT "Cloning and expression of a Leishmania donovani gene instructed by a
RT peptide isolated from major histocompatibility complex class II
RT molecules of infected macrophages.";
RL J. Exp. Med. 182:1423-1433(1995).
CC -!- SIMILARITY: BELONGS TO THE L14E FAMILY OF RIBOSOMAL PROTEINS.
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; X86551; CAA60246.1; -
DR InterPro: IPR000302; KOW_motif.
DR InterPro: IPR002784; Ribosomal_L14e.
DR Pfam; PF00467; KOW; 1.
DR Pfam; PF01929; Ribosomal_L14e; 1.
KW Ribosomal protein.
SQ SEQUENCE 175 AA; 19887 MW; A3P9AFF30D986814 CRC64;

Query Match          10.2%; Score 6; DB 1; Length 175;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AKRRMQ 37
DB 160 AKRRMQ 165
|||||

RESULT 28
FXV5_MOUSE
ID FXV5_MOUSE STANDARD; PRT; 178 AA.
AC P97808;
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE FXV5 domain-containing ion transport regulator 5 precursor
DE (Oncoprotein-induced protein 2) (Ion channel homolog RIC) (EP-8).
DE FXV5 OR OIR2.
GN Mus musculus (Mouse).
OS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BALB/C;
RX MEDLINE=97184476; PubMed=9032278;
RA Fu X., Kamps M.P.;
RT "p2a-pb1 induces aberrant expression of tissue-specific and
RT developmentally regulated genes when expressed in NIH 3T3
RT fibroblasts.";
RL Mol. Cell. Biol. 17:1503-1512(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Spleen;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaide I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawai H., Kohtsuki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).

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CC -! SUBCELLULAR LOCATION: Type I membrane protein (Potential).
CC -! TISSUE SPECIFICITY: SPLEEN, LUNG, SKELETAL MUSCLE, AND TESTIS.
CC -! DEVELOPMENTAL STAGE: EXHIBITS BIPHASIC EXPRESSION DURING
CC DEVELOPMENT.
CC -! SIMILARITY: BELONGS TO THE FXV5 FAMILY.
-----
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CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
-----
DR EMBL; U72680; AAB51040.1; -
DR EMBL; AK003068; BAB22545.1; -
DR MGD; MGI:1201785; Fxyd5.
DR InterPro: IPR000272; ATP1GL_PLM_MAT8.
DR Pfam; PF02038; ATP1GL_PLM_MAT8; 1.
DR PROSITE; PS01310; FXYD; 1.
KW Transmembrane; Signal; Ionic channel; Ion transport.
FT SIGNAL 1 21 POTENTIAL.
FT CHAIN 22 178 FXYD DOMAIN-CONTAINING ION TRANSPORT
REGULATOR 5.
FT DOMAIN 22 145 EXTRACELLULAR (POTENTIAL).
FT TRANSMEM 146 166 POTENTIAL.
FT DOMAIN 167 178 CYTOPLASMIC (POTENTIAL).
FT DOMAIN 88 134 PRO-RICH.
SQ SEQUENCE 178 AA; 19454 MW; 466FBF1E05D861C5 CRC64;

Query Match          10.2%; Score 6; DB 1; Length 178;
Best Local Similarity 100.0%; Pred. No. 44;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 13 RGQTPK 18
DB 20 RGQTPK 25
|||||

RESULT 29
CC42_CAEL
ID CC42_CAEL STANDARD; PRT; 188 AA.
AC Q05062;
DT 01-FEB-1994 (Rel. 28, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Cell division control protein 42 homolog (CDC42CE).
DE CDC-42 OR R07G3.1.
GN Caenorhabditis elegans.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditidae;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RX MEDLINE=93293845; PubMed=8514766;
RA Chen W., Lim H., Lim L.;
RA "The CDC42 homologue from Caenorhabditis elegans. Complementation of
RA yeast mutation.";
RL J. Biol. Chem. 268:13280-13285(1993).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Bristol N2;
RA Waterston R.;
RA Submitted (JUL-1995) to the EMBL/GenBank/DBJ databases.
CC -! DEVELOPMENTAL STAGE: HIGHEST LEVELS AT THE EMBRYONIC STAGE,
CC DECREASING PROGRESSIVELY DURING DEVELOPMENT, EXCEPT FOR AN
CC INCREASE AT THE L3 STAGE.
CC -! SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC CDC42 SUBFAMILY.
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CC EMBL; LI0078; AAA51433.1; .
 DR EMBL; U23452; AAK31543.1; ALT_INIT.
 DR PIR; A46578; A46578.
 DR HSSP; P21181; 1AM4.
 DR WormPep; R07G3.1; CE02020.
 DR InterPro; IPR003578; GTPase_Rho.
 DR InterPro; IPR001806; Ras_trnsmg.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00071; ras; 1.
 DR PRINTS; PR00449; RASTRNSFRMG.
 DR SMART; SM00174; RHO; 1.
 DR TIGRFAMS; TIGR00231; small_GTP; 1.
 KW GTP-binding; Lipoprotein; Cell cycle; Cell division; Prenylation.
 FT NP_BIND 7 14 GTP (BY SIMILARITY).
 FT NP_BIND 54 58 GTP (BY SIMILARITY).
 FT NP_BIND 112 115 GTP (BY SIMILARITY).
 FT DOMAIN 29 37 EFFECTOR REGION (BY SIMILARITY).
 FT LIPID 185 185 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 188 AA; 20823 MW; 873395896B681299 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEKKKK 27
 |||||
 DB 179 QEKKKK 184

RESULT 30
 RASK_MELGA
 ID RASK_MELGA STANDARD; PRT; 188 AA.
 AC P79800;
 DT 01-NOV-1997 (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35; Last sequence update)
 DT 16-OCT-2001 (Rel. 40; Last annotation update)
 DE Transforming protein p21 (K-Ras) (Ki-Ras).
 GN KRAS.
 OS Meleagris gallopavo (Common turkey).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Aves; Neognathae; Galliformes; Meleagrididae; Meleagris.
 OX NCBI_TaxID=9103;
 [1]
 RN SEQUENCE FROM N.A.
 RC TISSUE=Splice;
 RX MEDLINE=97080492; PubMed=8921837;
 RA Chajut A., Gazit A., Yaniv A.;
 RT "The turkey c-rapLA proto-oncogene is expressed via two distinct
 RT promoters.";
 RL Gene 177:7-10(1996).
 CC 1- FUNCTION: RAS PROTEINS BIND GDP/GTP AND POSSESS INTRINSIC GTPASE
 CC ACTIVITY.
 CC 1- ENZYME REGULATION: ALTERNATE BETWEEN AN INACTIVE FORM BOUND TO GDP
 CC AND AN ACTIVE FORM BOUND TO GTP. ACTIVATED BY A GUANINE
 CC NUCLEOTIDE-EXCHANGE FACTOR (GEF) AND INACTIVATED BY A GTPASE-
 CC ACTIVATING PROTEIN (GAP).
 CC 1- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RAS FAMILY.
 CC
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 CC or send an email to license@isb-sib.ch).

EMBL; X85754; CAA59755.1; .

DR HSSP; P01112; 1PLL.
 DR InterPro; IPR003577; GTPase_Ras.
 DR InterPro; IPR001230; Prenyl_site.
 DR InterPro; IPR001806; Ras_trnsmg.
 DR InterPro; IPR005225; Small_GTP.
 DR Pfam; PF00071; ras; 1.
 DR PRINTS; PR00449; RASTRNSFRMG.
 DR SMART; SM00173; RAS; 1.
 DR TIGRFAMS; TIGR00231; small_GTP; 1.
 KW Proto-oncogene; GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 10 17 GTP (BY SIMILARITY).
 FT NP_BIND 57 61 GTP (BY SIMILARITY).
 FT NP_BIND 116 119 GTP (BY SIMILARITY).
 FT DOMAIN 32 40 EFFECTOR REGION (BY SIMILARITY).
 FT LIPID 185 185 FARNESYL (BY SIMILARITY).
 SQ SEQUENCE 188 AA; 21452 MW; AAB6C319BB259865 CRC64;
 Query Match 10.2%; Score 6; DB 1; Length 188;
 Best Local Similarity 100.0%; Pred. No. 46;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
 |||||
 DB 176 KKKKKT 181

RESULT 31
 PAPH_ECOLI
 ID PAPH_ECOLI STANDARD; PRT; 195 AA.
 AC P07111;
 DT 01-APR-1988 (Rel. 07, Created)
 DT 01-APR-1988 (Rel. 07; Last sequence update)
 DT 15-DEC-1998 (Rel. 37; Last annotation update)
 DE PAP fimbrial minor pilin protein precursor.
 GN PAPH.
 OS Escherichia coli.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Escherichia.
 OX NCBI_TaxID=562;
 [1]
 RN SEQUENCE FROM N.A.
 RC STRAIN=J96;
 RX MEDLINE=87187619; PubMed=2882856;
 RA Baga M., Norgren M., Normark S.;
 RT "Biogenesis of E. coli Pap pili: paph, a minor pilin subunit involved
 RT in cell anchoring and length modulation.";
 RL Cell 49:241-251(1987).
 [2]
 RN SEQUENCE FROM N.A.
 RC STRAIN=J96;
 RX MEDLINE=93023852; PubMed=1357526;
 RA Marklund B.-I., Tennent J.M., Garcia E., Hamers A., Baga M.,
 RA Lindberg F., Gastra W., Normark S.;
 RT "Horizontal gene transfer of the Escherichia coli pap and prs pili
 RT operons as a mechanism for the development of tissue-specific
 RT adhesive properties.";
 RL Mol. Microbiol. 6:2225-2242(1992).
 [3]
 RN SEQUENCE OF 149-195 FROM N.A.
 RC STRAIN=J96;
 RX MEDLINE=88216160; PubMed=2897064;
 RA Norgren M., Baga M., Tennent J.M., Normark S.;
 RT "Nucleotide sequence, regulation and functional analysis of the papC
 RT gene required for cell surface localization of Pap pili of
 RT uropathogenic Escherichia coli.";
 RL Mol. Microbiol. 1:169-178(1987).
 CC 1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
 CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
 CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
 CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
 CC 1- FUNCTION: PAPH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL.
 CC IN ADDITION THE STOICHIOMETRIC RELATIONSHIP BETWEEN PAPH AND
 CC PAPA DETERMINES THE PILUS LENGTH.

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (39)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (40)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1633

Query Match 10.2%: Score 6; DB 10; Length 43;
Best Local Similarity 100.0%; Pred. No. 25;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKKK 28
Db 1 EKKKKK 6

RESULT 21
US-09-764-869-926
Sequence 926, Application US/09764869
Patent No. US20020061521A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PC007
CURRENT APPLICATION NUMBER: US/09/764,869
CURRENT FILING DATE: 2001-01-17
Prior application data removed - refer to PALM or file wrapper
NUMBER OF SEQ ID NOS: 2442
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 926
LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-869-926

Query Match 10.2%: Score 6; DB 10; Length 45;
Best Local Similarity 100.0%; Pred. No. 26;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 23 EKKKKK 28
Db 33 EKKKKK 38

RESULT 22
US-09-925-299-1098
Sequence 1098, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05883
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124,270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1098
LENGTH: 48
TYPE: PRT
ORGANISM: Homo sapiens
US-09-925-299-1098

Query Match 10.2%: Score 6; DB 10; Length 48;
Best Local Similarity 100.0%; Pred. No. 27;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 KKKKKT 29

Db 7 KKKKKT 12

RESULT 23
US-09-983-802-479
Sequence 479, Application US/09983802
Publication No. US20030022185A1
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/983,802
CURRENT FILING DATE: 2001-10-25
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/2227,357
PRIOR FILING DATE: EARLIER FILING DATE: 1999-01-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: PCT/US98/13684
PRIOR FILING DATE: EARLIER FILING DATE: 1998-07-07
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,926
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,793
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,925
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,929
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,803
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,732
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,931
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,932
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,916
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,930
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,918
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,920
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,733
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/052,795
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,919
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/051,928
PRIOR FILING DATE: EARLIER FILING DATE: 1997-07-08
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,722
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,723
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,948
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,949
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,953
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,950
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,947
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,964
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/056,360
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,684
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,984
PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/055,954

RESULT 17
US-09-764-877-1043
; Sequence 1043, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1043
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1043

Query Match 10.2%; Score 6; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
Db 10 EKKKKK 15

RESULT 18
US-09-925-300-1820
; Sequence 1820, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruden,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1820
; LENGTH: 36
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (1)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1820

Query Match 10.2%; Score 6; DB 10; Length 36;
Best Local Similarity 100.0%; Pred. No. 21;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
Db 17 EKKKKK 22

RESULT 19
US-09-925-301-1640
; Sequence 1640, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1640
; LENGTH: 37
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (30)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (32)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (34)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1640

Query Match 10.2%; Score 6; DB 10; Length 37;
Best Local Similarity 100.0%; Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
Db 10 EKKKKK 15

RESULT 20
US-09-925-301-1633
; Sequence 1633, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1633
; LENGTH: 43
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (31)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (35)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (38)

OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (23)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (28)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1319

Query Match 10.2%; Score 6; DB 10; Length 28;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKK 29
DB 10 KKKKK 15

RESULT 14
US-09-071-838-189
Sequence 189, Application US/09071838
Patent No. US20020152501A1
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Mir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegari, Ramin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: Nucleic Acids That Control Seed and
TITLE OF INVENTION: Fruit Development in Plants
NUMBER OF SEQUENCES: 324
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: US/09/071, 838
APPLICATION NUMBER: US/09/071, 838
FILING DATE: 01-MAY-1998
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Bastian, Kevin L.
REGISTRATION NUMBER: 34,774
REFERENCE/DOCKET NUMBER: 023070-086100US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 189:
SEQUENCE CHARACTERISTICS:
LENGTH: 29 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-071-838-189

Query Match 10.2%; Score 6; DB 10; Length 29;
Best Local Similarity 100.0%; Pred. No. 18;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKK 53
DB 1 TFGKK 6

RESULT 15
US-09-764-846-248
Sequence 248, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: P212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 248
LENGTH: 31
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-846-248

Query Match 10.2%; Score 6; DB 10; Length 31;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
DB 5 EKKKK 10

RESULT 16
US-09-925-299-1474
Sequence 1474, Application US/09925299
Patent No. US20020055627A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA102
CURRENT APPLICATION NUMBER: US/09/925,299
CURRENT FILING DATE: 2001-08-10
Prior application number: PCT/US00/05883
Prior filing date: 2000-03-08
Prior application number: 60/124,270
Prior filing date: 1999-03-12
NUMBER OF SEQ ID NOS: 1556
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1474
LENGTH: 32
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (25)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (30)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
NAME/KEY: SITE
LOCATION: (31)
OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1474

Query Match 10.2%; Score 6; DB 10; Length 32;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
DB 17 EKKKK 22

```
; INFORMATION FOR SEQ ID NO: 201:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 16 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
US-09-438-486-201

Query Match
Best Local Similarity 100.0%; Score 6; DB 9; Length 16;
Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
Db 8 EKKKK 13

RESULT 11
US-09-764-869-729
; Sequence 729, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 729
; LENGTH: 17
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-869-729

Query Match
Best Local Similarity 100.0%; Score 6; DB 10; Length 17;
Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
Db 10 EKKKK 15

RESULT 12
US-09-864-761-41097
; Sequence 41097, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharron G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aeomica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
```

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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 41097
; LENGTH: 24
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC013746.4
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 3.8
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 2.7
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 5.6
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 5.7
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 5.8
; OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 3.6
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.8
US-09-864-761-41097

Query Match
Best Local Similarity 100.0%; Score 6; DB 10; Length 24;
Pred. No. 16;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
Db 6 EKKKK 11

RESULT 13
US-09-925-299-1319
; Sequence 1319, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1319
; LENGTH: 28
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (17)
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;; CURRENT FILING DATE: 2001-08-31
;; PRIOR APPLICATION NUMBER: 09/041,990
;; PRIOR FILING DATE: 2001-01-13
;; PRIOR APPLICATION NUMBER: 08/771,212
;; PRIOR FILING DATE: 1996-12-20
;; PRIOR APPLICATION NUMBER: 08/531,319
;; PRIOR FILING DATE: 1996-04-11
;; NUMBER OF SEQ ID NOS: 89
;; SOFTWARE: PatentIn Ver. 2.1
;; SEQ ID NO: 87
;; LENGTH: 15
;; TYPE: PRT
;; ORGANISM: Artificial Sequence
;; FEATURE:
;; OTHER INFORMATION: Description of Artificial Sequence: Peptide that
;; OTHER INFORMATION: corresponds to the C-termini of Frase or Ggtase
;; OTHER INFORMATION: substrates
US-09-945-249-87

Query Match 10.2%; Score 6; DB 9; Length 15;
Best Local Similarity: 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
Db 6 EKKKK 11

RESULT 9
US-09-843-676-201

;; Sequence 201, Application US/09843676
;; Patent No. US20020164786A1

;; GENERAL INFORMATION:

;; APPLICANT: Cech, Thomas R.

;; Linger, Joachim

;; Nakamura, Toru

;; Chapman, Karen B.

;; Morin, Gregg B.

;; Harley, Calvin

;; Andrews, William H.

;; TITLE OF INVENTION: NO. US20020164786A1 Telomerase

;; NUMBER OF SEQUENCES: 225

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP

;; STREET: Two Embarcadero Center, 8th Floor

;; CITY: San Francisco

;; STATE: California

;; COUNTRY: United States of America

;; ZIP: 94111

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; OPERATING SYSTEM: IBM PC compatible

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/843,676

;; FILING DATE: 26-APR-2001

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US/08/854,050

;; FILING DATE: 09-MAY-1997

;; APPLICATION NUMBER: US 08/846,017

;; FILING DATE: 25-APR-1997

;; APPLICATION NUMBER: US 08/844,419

;; FILING DATE: 18-APR-1997

;; APPLICATION NUMBER: US 08/724,643

;; FILING DATE: 01-OCT-1996

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Apple, Randolph T.

;; REGISTRATION NUMBER: 36,429

;; REFERENCE/DOCKET NUMBER: 015389-002930US

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 576-0200

;; TELEFAX: (415) 576-0300
;; INFORMATION FOR SEQ ID NO: 201:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 16 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-09-843-676-201

Query Match 10.2%; Score 6; DB 9; Length 16;
Best Local Similarity: 100.0%; Pred. No. 11;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
Db 8 EKKKK 13

RESULT 10
US-09-438-486-201

;; Sequence 201, Application US/09438486

;; Publication No. US20030009019A1

;; GENERAL INFORMATION:

;; APPLICANT: Cech, Thomas R.

;; Linger, Joachim

;; Nakamura, Toru

;; Chapman, Karen B.

;; Morin, Gregg B.

;; Harley, Calvin

;; Applicant: Andrews, William H.

;; TITLE OF INVENTION: NO. US20030009019A1 Telomerase

;; NUMBER OF SEQUENCES: 223

;; CORRESPONDENCE ADDRESS:

;; ADDRESSEE: Townsend and Townsend and Crew LLP

;; STREET: Two Embarcadero Center, 8th Floor

;; CITY: San Francisco

;; STATE: California

;; COUNTRY: United States of America

;; ZIP: 94111-3834

;; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk

;; OPERATING SYSTEM: IBM PC compatible

;; SOFTWARE: PatentIn Release #1.0, Version #1.30

;; CURRENT APPLICATION DATA:

;; APPLICATION NUMBER: US/09/438,486

;; FILING DATE: 12-NOV-1999

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/851,843

;; FILING DATE: 06-MAY-1997

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/846,017

;; FILING DATE: 25-APR-1997

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/844,419

;; FILING DATE: 18-APR-1997

;; CLASSIFICATION: 536

;; PRIOR APPLICATION DATA:

;; APPLICATION NUMBER: US 08/724,643

;; FILING DATE: 01-OCT-1996

;; CLASSIFICATION: 536

;; ATTORNEY/AGENT INFORMATION:

;; NAME: Apple, Randolph T.

;; REGISTRATION NUMBER: 36,429

;; REFERENCE/DOCKET NUMBER: 015389-002931US

;; TELECOMMUNICATION INFORMATION:

;; TELEPHONE: (415) 576-0200

;; TELEFAX: (415) 576-0300

OY 23 EKKKKKT 29
|||
Db 21 EKKKKKT 27

RESULT 4
US-09-764-877-1759
; Sequence 1759, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; PRIOR FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1759
; LENGTH: 121
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-877-1759

Query Match 11.9%; Score 7; DB 10; Length 121;
Best Local Similarity 100.0%; Pred. No. 6.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
|||
Db 114 EKKKKKT 120

RESULT 5
US-09-774-639-155
; Sequence 155, Application US/09774639
; Publication No. US20030003555A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 90 Human Secreted Proteins
; FILE REFERENCE: P2013P1
; CURRENT APPLICATION NUMBER: US/09/774,639
; PRIOR FILING DATE: 2001-07-09
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 09/244,112
; PRIOR FILING DATE: EARLIER FILING DATE: 1999-02-04
; NUMBER OF SEQ ID NOS: 371
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 155
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-774-639-155

Query Match 11.9%; Score 7; DB 9; Length 227;
Best Local Similarity 100.0%; Pred. No. 11;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
|||
Db 220 EKKKKKT 226

RESULT 6
US-10-014-717-5
; Sequence 5, Application US/10014717
; Publication No. US20020192778A1
; GENERAL INFORMATION:
; APPLICANT: Schupp, Thomas
; APPLICANT: Ligon, James
; APPLICANT: Molnar, Istvan
; APPLICANT: Zirkle, Ross
; APPLICANT: Cyr, Devon
; APPLICANT: Goerlach, Joern

; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
; FILE REFERENCE: 4-30582A
; CURRENT APPLICATION NUMBER: US/10/014,717
; PRIOR FILING DATE: 2001-11-13
; PRIOR APPLICATION NUMBER: US/09/335,409
; PRIOR FILING DATE: 1999-06-17
; NUMBER OF SEQ ID NOS: 30
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 5
; LENGTH: 7257
; TYPE: PRT
; ORGANISM: Sorangium cellulosum
US-10-014-717-5

Query Match 11.9%; Score 7; DB 9; Length 7257;
Best Local Similarity 100.0%; Pred. No. 1.7e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAGK 11
|||
Db 7250 SLARAGK 7256

RESULT 7
US-09-983-067-1
; Sequence 1, Application US/09983067
; Patent No. US20020123101A1
; GENERAL INFORMATION:
; APPLICANT: INOUE, Akio
; APPLICANT: SHIMIZU, Yoshihiro
; APPLICANT: UEDA, Takuya
; TITLE OF INVENTION: Process for Producing Peptides By Using In Vitro
; TITLE OF INVENTION: Transcription/Translation System
; FILE REFERENCE: 1752-0151P
; CURRENT APPLICATION NUMBER: US/09/983,067
; PRIOR FILING DATE: 2001-10-23
; PRIOR APPLICATION NUMBER: JP 294795/2001
; PRIOR FILING DATE: 2001-09-26
; PRIOR APPLICATION NUMBER: JP 227094/2001
; PRIOR FILING DATE: 2001-07-27
; PRIOR APPLICATION NUMBER: JP 6910/2001
; PRIOR FILING DATE: 2001-01-15
; PRIOR APPLICATION NUMBER: JP 401417/2000
; PRIOR FILING DATE: 2000-12-28
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 14
; TYPE: PRT
; ORGANISM: Bovine sp.
US-09-983-067-1

Query Match 10.2%; Score 6; DB 10; Length 14;
Best Local Similarity 100.0%; Pred. No. 10;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKK 28
|||
Db 9 EKKKKK 14

RESULT 8
US-09-945-249-87
; Sequence 87, Application US/09945249
; Patent No. US20020168748A1
; GENERAL INFORMATION:
; APPLICANT: BERLIN, VIVIAN
; APPLICANT: DAMAGNEZ, VERONIQUE
; APPLICANT: SMITH, SUSAN E.
; TITLE OF INVENTION: ASSAYS AND REAGENTS FOR IDENTIFYING ANTI-FUNGAL AGENTS,
; FILE REFERENCE: MIV-074_06
; CURRENT APPLICATION NUMBER: US/09/945,249

```
APPLICANT: Hanzel, David K.
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
FILE REFERENCE: Aeonica-X-1
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US/09/864,761
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263,6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 35333
LENGTH: 118
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC009704.2
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 19
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 8.8
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 18
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 9.3
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 4.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 81
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 12
OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 30
OTHER INFORMATION: SWISSPROT HIT: P35544, EVALU 4.00e-23
OTHER INFORMATION: EST_HUMAN HIT: BF347807.1, EVALU 6.00e-47
US-09-864-761-35333

Query Match 47.5% Score 28; DB 10; Length 118;
Best Local Similarity 100.0%; Pred. No. 2.8e-19;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
QY 1 KKHGSLARAGKVRGQTPKVAKEKKKK 28
DB 56 KKHGSLARAGKVRGQTPKVAKEKKKK 83
```

```
RESULT 3
US-09-864-761-39484
Sequence 39484, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: Chen, Wensheng
TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FC
FILE REFERENCE: Aeonica-X-1
CURRENT FILING DATE: 2001-05-23
PRIORITY APPLICATION NUMBER: US/09/864,761
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/180,312
PRIORITY FILING DATE: 2000-02-04
PRIORITY APPLICATION NUMBER: US 60/207,456
PRIORITY FILING DATE: 2000-05-26
PRIORITY APPLICATION NUMBER: US 09/632,366
PRIORITY FILING DATE: 2000-08-03
PRIORITY APPLICATION NUMBER: GB 24263,6
PRIORITY FILING DATE: 2000-10-04
PRIORITY APPLICATION NUMBER: US 60/236,359
PRIORITY FILING DATE: 2000-09-27
PRIORITY APPLICATION NUMBER: PCT/US01/00666
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00667
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00664
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00669
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00665
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00668
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00663
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00662
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00661
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: PCT/US01/00670
PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
SEQ ID NO 39484
LENGTH: 62
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO AC005598.6
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 7.1
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 7.4
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 7.2
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 6.7
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 6.7
US-09-864-761-39484

Query Match 11.9% Score 7; DB 10; Length 62;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 21:31:19 : Search time 11 Seconds
(without alignments)
118.908 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KVHSLARAGKVRGQTPKVA.....RRFVNVVPTFGKKKGNPNS 59

Scoring table:

Gapop 60.0 , Gapext 60.0

Searched: 129505 seqs, 22169297 residues

Word size : 0

Total number of hits satisfying chosen parameters: 129505

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB pep:*
- 2: /cgn2_6/ptodata/2/pubppaa/PCF_NEW_PUB pep:*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB pep:*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB pep:*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB pep:*
- 6: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB pep:*
- 7: /cgn2_6/ptodata/2/pubppaa/PCFUS_PUBCOMB pep:*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB pep:*
- 9: /cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB pep:*
- 10: /cgn2_6/ptodata/2/pubppaa/US09_PUBCOMB pep:*
- 11: /cgn2_6/ptodata/2/pubppaa/US10_NEW_PUB pep:*
- 12: /cgn2_6/ptodata/2/pubppaa/US10_PUBCOMB pep:*
- 13: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB pep:*
- 14: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	170	US-09-925-301-994	Sequence 994, App
2	28	47.5	118	US-09-864-761-35333	Sequence 35333, A
3	7	11.9	62	US-09-864-761-39484	Sequence 39484, A
4	7	11.9	121	US-09-764-877-1759	Sequence 1759, Ap
5	7	11.9	227	US-09-774-639-155	Sequence 155, App
6	7	11.9	7257	US-10-014-717-5	Sequence 5, Appl1
7	6	10.2	14	US-09-983-067-1	Sequence 1, Appl1
8	6	10.2	15	US-09-945-249-87	Sequence 87, Appl
9	6	10.2	16	US-09-843-676-201	Sequence 201, App
10	6	10.2	16	US-09-438-486-201	Sequence 201, App
11	6	10.2	17	US-09-764-869-729	Sequence 729, App
12	6	10.2	24	US-09-864-761-41097	Sequence 41097, A
13	6	10.2	28	US-09-925-299-1319	Sequence 1319, Ap
14	6	10.2	29	US-09-071-838-189	Sequence 189, App
15	6	10.2	31	US-09-764-846-246	Sequence 248, App
16	6	10.2	32	US-09-925-299-1474	Sequence 1474, Ap
17	6	10.2	36	US-09-764-877-1043	Sequence 1043, App
18	6	10.2	36	US-09-925-300-1820	Sequence 1820, Ap
19	6	10.2	37	US-09-925-301-1640	Sequence 1640, Ap

20	6	10.2	43	10	US-09-925-301-1633	Sequence 1633, Ap
21	6	10.2	45	10	US-09-764-869-926	Sequence 926, App
22	6	10.2	48	10	US-09-925-299-1098	Sequence 1098, Ap
23	6	10.2	51	9	US-09-983-802-479	Sequence 479, App
24	6	10.2	52	10	US-09-764-869-1228	Sequence 1228, Ap
25	6	10.2	55	10	US-09-764-855-113	Sequence 113, App
26	6	10.2	57	10	US-09-764-847-601	Sequence 601, App
27	6	10.2	57	10	US-09-864-761-47593	Sequence 47593, A
28	6	10.2	59	10	US-09-864-761-47812	Sequence 47812, A
29	6	10.2	60	9	US-09-989-919-118	Sequence 118, App
30	6	10.2	60	10	US-09-925-300-1198	Sequence 1198, App
31	6	10.2	62	10	US-09-925-301-1475	Sequence 1475, Ap
32	6	10.2	63	9	US-10-117-604-2	Sequence 2, Appl1
33	6	10.2	63	10	US-09-764-846-260	Sequence 260, App
34	6	10.2	64	10	US-09-864-761-45501	Sequence 45501, A
35	6	10.2	66	10	US-09-764-846-224	Sequence 224, App
36	6	10.2	66	10	US-09-764-877-1089	Sequence 1089, App
37	6	10.2	67	10	US-09-867-550-284	Sequence 284, App
38	6	10.2	68	9	US-09-201-936-18	Sequence 18, Appl
39	6	10.2	68	9	US-09-201-936-19	Sequence 19, Appl
40	6	10.2	68	10	US-09-764-846-191	Sequence 191, App
41	6	10.2	69	10	US-09-925-299-1340	Sequence 1340, Ap
42	6	10.2	72	10	US-09-764-846-179	Sequence 179, App
43	6	10.2	72	10	US-09-925-300-1105	Sequence 1105, Ap
44	6	10.2	73	10	US-09-764-846-242	Sequence 242, App
45	6	10.2	75	10	US-09-833-067-9	Sequence 9, Appl1

ALIGNMENTS

RESULT 1
US-09-925-301-994
Sequence 994, Application US/09925301
Patent No. US20020052308A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
FILE REFERENCE: PA106
CURRENT APPLICATION NUMBER: US/09/925, 301
CURRENT FILING DATE: 2001-08-10
PRIOR APPLICATION NUMBER: PCT/US00/05882
PRIOR FILING DATE: 2000-03-08
PRIOR APPLICATION NUMBER: 60/124, 270
PRIOR FILING DATE: 1999-03-12
NUMBER OF SEQ ID NOS: 1694
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 994
LENGTH: 170
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (5)
OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-994

Query Match 100.0%; Score 59; DB 10; Length 170;
Best Local Similarity 100.0%; Pred. No. 9.3e-48;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHSLARAGKVRGQTPKVAOEKKKKTKGRKRMQYRRFVNVPTFGKKKGNPNS 59
|||||
Db 112 KVHSLARAGKVRGQTPKVAOEKKKKTKGRKRMQYRRFVNVPTFGKKKGNPNS 170

RESULT 2
US-09-864-761-35333
Sequence 35333, Application US/09864761
Patent No. US20020048763A1
GENERAL INFORMATION:
APPLICANT: Penn, Sharon G.
APPLICANT: Rank, David R.

```
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: STRAINS OF E. COLI THAT CAUSE INFECTION OF THE HUMAN
CC URINARY TRACT PRODUCE PAP-PIII WHICH ARE HAIR-LIKE APPENDAGES
CC CONSISTING OF ABOUT 1000 HELICALLY ARRANGED SUBUNITS OF THE
CC PROTEIN PAPA. THESE PIII MEDIANE BINDING TO DIGALACTOSIDE-
CC CONTAINING GLYCOLIPIDS PRESENT ON THE EPITHELIAL CELLS WHICH
CC LINE THE URINARY TRACT.
CC -----
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CC -----
DR EMBL; Y00529; CAAB6587.1; -
DR EMBL; M16202; AAA24286.1; -
DR EMBL; X61239; CAAB43563.1; -
DR PIR; A27021; YOECPH.
DR InterPro: IPR000259; Fimbrial.
DR Pfam; PF00419; Fimbrial; 1.
KW Fimbrin; Signal.
FT SIGNAL 1 22
FT CHAIN 23 195 PAP FIMBRIAL MINOR PILIN PROTEIN.
FT DISULFID 58 97 PROBABLE.
SQ SEQUENCE 195 AA; 21835 MW; D2120FCSDA063169 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAGV 12
DB 148 ARAGV 153

RESULT 32
PRSH_ECOLI STANDARD; PRT; 195 AA.
ID PRSH_ECOLI
AC P42185;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-DEC-1998 (Rel. 37, Last annotation update)
DE PRS fimbrial minor pilin protein precursor.
CN PRSH.
OS Escherichia coli.
OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
OC Escherichia.
OX NCBI_Taxid=562;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=1442;
RX MEDLINE=93023852; PubMed=1357526;
RA Marklund B., Tennent J.M., Garcia E., Hamers A., Baga M.,
RA Lindberg F., Gaastra W., Normark S.;
RA "Horizontal gene transfer of the Escherichia coli pap and prs pili
RT operators as a mechanism for the development of tissue-specific
RT adhesive properties."
RL Mol. Microbiol. 6:2225-2242(1992).
CC -1- FUNCTION: FIMBRIAE (ALSO CALLED PILI), POLAR FILAMENTS RADIATING
CC FROM THE SURFACE OF THE BACTERIUM TO A LENGTH OF 0.5-1.5
CC MICROMETERS AND NUMBERING 100-300 PER CELL, ENABLE BACTERIA TO
CC COLONIZE THE EPITHELIUM OF SPECIFIC HOST ORGANS.
CC -1- FUNCTION: PRSH SEEMS TO ANCHOR THE PILUS TO THE BACTERIAL CELL.
CC IN ADDITION THE STOICHIOMETRIC RELATIONSHIP BETWEEN PRSH AND
CC PRSA DETERMINES THE PILUS LENGTH.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; X62157; CAAB4082.1; -
DR InterPro: IPR000259; Fimbrial.
DR Pfam; PF00419; Fimbrial; 1.
KW Fimbrin; Signal.
FT SIGNAL 1 22 BY SIMILARITY.
FT CHAIN 23 195 PRS FIMBRIAL MINOR PILIN PROTEIN.
FT DISULFID 58 97 PROBABLE.
SQ SEQUENCE 195 AA; 21837 MW; A5065BEF93D5861B CRC64;

Query Match 10.2%; Score 6; DB 1; Length 195;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAGV 12
DB 148 ARAGV 153

RESULT 33
RMRP_YEAST STANDARD; PRT; 198 AA.
ID RMRP_YEAST
AC P40993;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last annotation update)
DE RNase MRP protein component SNM1.
DE SNM1 OR YDR478W OR D8035.21.
OS Saccharomyces cerevisiae (Baker's yeast).
OC Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX NCBI_Taxid=4932;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=S288C;
RX MEDLINE=95047399; PubMed=7958920;
RA Schmitt M.E., Clayton D.A.;
RT "Characterization of a unique protein component of yeast RNase MRP:
RT an RNA-binding protein with a zinc-cluster domain."
RL Genes Dev. 8:2617-2628(1994).
RN [2]
RP SEQUENCE FROM N.A.
RA Dietrich F.S., Mulligan J., Allen E., Araujo R., Aviles E.,
RA Berno A., Carpenter J., Chen E., Cherry J.M., Chung E., Duncan M.,
RA Hunnicke-Smith S., Hyman R., Komp C., Lashkari D., Lew H., Lin D.,
RA Mosedale D., Nakahara K., Namath A., Oefner P., Oh C., Petel F.X.,
RA Roberts D., Schramm S., Schroeder M., Shogren T., Shroff N.,
RA Winant A., Yelton M., Botstein D., Davis R.W.;
RA submitted (AUG-1995) to the EMBL/GenBank/DBJ databases.
RL SNM1.
CC -1- FUNCTION: ESSENTIAL COMPONENT OF THE MRP RIBONUCLEOPROTEIN
CC ENDORIBONUCLEASE THAT CLEAVES MITOCHONDRIAL PRIMER RNA SEQUENCES.
CC -1- SUBUNIT: HOMODIMER (POTENTIAL).
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; Z37982; CAAB6054.1; -
DR EMBL; U33050; AAB64905.1; -
DR PIR; S48236; S48236.
DR SGD: S0002886; SNM1.
KW Hydroxylase; Nuclease; RNA-binding.
FT DOMAIN 136 198 LYS/SER-RICH.
SQ SEQUENCE 198 AA; 22541 MW; 67C262585D3BEA3A CRC64;

Query Match 10.2%; Score 6; DB 1; Length 198;
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Best Local Similarity 100.0%; Pred. No. 48;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 45 VVPTFG 50
Db 122 VVPTFG 127

RESULT 34

RASM_HUMAN
ID RASM_HUMAN STANDARD: PRT; 208 AA.
AC 014807;
DT 30-MAY-2000 (Rel. 39, Created)
DT 30-MAY-2000 (Rel. 39, Last sequence update)
DT 15-JUN-2002 (Rel. 41, Last annotation update)
DE Ras-related protein M-Ras (Ras-related protein R-Ras3).
GN MRAS OR RAS3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=lung;
RA Kimmelman A., Tolacheva T., Lorenzi M.V., Osada M., Chan A.M.-L.,
RT Identification and characterization of R-ras3: a novel member of the
RT Ras gene family with a non-ubiquitous pattern of tissue
RT distribution.
RL Oncogene 15:2675-2686(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RA Louhed J., Grasso L., de Smet C., van Roost E., Wildmann C.,
RT Interleukin-9-induced expression of M-Ras/R-Ras3 oncogene in T-helper
RT clones.
RL Blood 94:1701-1710(1999).
CC -1- FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NOVEL
CC UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY
CC ACTIVATES THE MAP KINASE PATHWAY.
CC -1- TISSUE SPECIFICITY: EXPRESSION HIGHLY RESTRICTED TO THE BRAIN AND
CC HEART.
CC -1- INDUCTION: BY INTERLEUKIN-9, BUT NOT BY IL-2 OR IL-4.
CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
CC -----
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CC -----
CC EMBL: AF022080; AAC52085.1; -;
CC EMBL: AF043938; AAD02287.1; -;
CC HSSP: P01112; 1PLK.
CC Genew: HGNC:7227; MRAS.
DR InterPro: IPR001230; GTPase_Ras.
DR InterPro: IPR001806; Prenyl_site.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00071; ras; 1.
DR PRINTS: PR00449; RASTRNSFRMNG.
DR SMART: SM00173; RAS; 1.
DR TIGRFS: TIGR00231; small_GTP; 1.
KW GTP-binding; Prenylation; Lipoprotein.
FT NP_BIND 20 27
FT NP_BIND 67 71 GTP (BY SIMILARITY).
FT NP_BIND 126 129 GTP (BY SIMILARITY).
FT DOMAIN 42 50 EFFECTOR REGION (BY SIMILARITY).
FT DOMAIN 185 191 POLY-LYS.

FT LIPID 205 205 GERANYL-GERANYL (BY SIMILARITY).
SQ SEQUENCE 208 AA; 23846 MW; 0B2B55AFA96B3EC4 CRC64;

Query Match 10.2%; Score 6; DB 1; Length 208;
Best Local Similarity 100.0%; Pred. No. 51;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKKT 29
Db 185 KKKKKT 190

RESULT 35

RASM_MOUSE
ID RASM_MOUSE STANDARD: PRT; 208 AA.
AC 008989;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE Ras-related protein M-Ras (Ras-related protein R-Ras3) (Muscle and
DE microspikes Ras) (X-Ras).
GN MRAS OR XRAS.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=98055615; PubMed=9395237;
RA Matsumoto K., Asano T., Endo T.;
RT Novel small GTPase M-Ras participates in reorganization of actin
RT cytoskeleton.
RL Oncogene 15:2409-2417(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6;
RA Louhed J., Grasso L., de Smet C., van Roost E., Wildmann C.,
RT Interleukin-9-induced expression of M-Ras/R-Ras3 oncogene in T-helper
RT clones.
RL Blood 94:1701-1710(1999).
RN [3]
RP SEQUENCE FROM N.A.
RA Leslie K.B., Schrader J.W.;
RT Characterization of a transforming, novel ras-related molecule.
RL Submitted (OCT-1997) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NOVEL
CC UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY
CC ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).
CC -1- SIMILARITY: TO RAS PROTEINS. BELONGS TO THE R-RAS SUB-FAMILY.
CC -----
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CC -----
CC EMBL: AB004879; BAA20538.1; -;
CC EMBL: AF043581; AAD02277.1; -;
CC EMBL: AF031159; AAD01926.1; -;
CC HSSP: P01112; 1PLK.
CC MGD: MGI:1100856; Mras.
DR InterPro: IPR001230; GTPase_Ras.
DR InterPro: IPR001806; Prenyl_site.
DR InterPro: IPR005225; Small_GTP.
DR Pfam: PF00071; ras; 1.
DR PRINTS: PR00449; RASTRNSFRMNG.
DR SMART: SM00173; RAS; 1.
DR TIGRFS: TIGR00231; small_GTP; 1.

KM GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 20 27 GTP (BY SIMILARITY).
 FT NP_BIND 67 71 GTP (BY SIMILARITY).
 FT NP_BIND 126 129 GTP (BY SIMILARITY).
 FT DOMAIN 42 50 EFFECTOR REGION (BY SIMILARITY).
 FT DOMAIN 185 191 POLY-LYS.
 FT LIPID 205 205 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 208 AA; 23901 MW; 975CFDD1FDF37FCF CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKK 29
 185 KKKKK 190

Db 185 KKKKK 190

RESULT 36
 RASM RAT
 ID RASM RAT STANDARD; PRT; 208 AA.
 AC P97538; 009021; (Rel. 35, Created)
 DT 01-NOV-1997 (Rel. 35, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE Ras-related protein M-Ras (Ras-related protein R-Ras3).
 GN MRAS OR RRAS3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Brain;
 RX MEDLINE=98055615; PubMed=9395237;
 RA Matsuno K, Asano T, Endo T.;
 RT "Novel small GTPase M-Ras participates in reorganization of actin
 cytoskeleton";
 RL Oncogene 15:2409-2417(1997).
 RN [2]
 RP REVISION TO 136.
 RA Endo T.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: MAY SERVE AS AN IMPORTANT SIGNAL TRANSDUCER FOR A NOVEL
 UPSTREAM STIMULI IN CONTROLLING CELL PROLIFERATION. WEAKLY
 ACTIVATES THE MAP KINASE PATHWAY (BY SIMILARITY).
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN SKELETAL MUSCLE CELLS.
 CC -1- SIMILARITY: TO RAS PROTEINS, BELONGS TO THE R-RAS SUB-FAMILY.
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 or send an email to license@sib-sib.ch).

CC EMBL; D89863; BAA20531.1; -
 CC HSSP; P01112; 1PLK.
 DR InterPro: IPR003577; GTPase_Ras.
 DR InterPro: IPR001230; Prenyl_site.
 DR InterPro: IPR001806; Ras_transfmg.
 DR InterPro: IPR005225; Small_GTP.
 DR Pfam: PF00071; Ras; 1.
 DR PRINTS: PR00449; RASTRNSFRMNG.
 DR SMART: SM00173; Ras; 1.
 DR TIGRFAMs: TIGR00231; small_gtp; 1.
 KM GTP-binding; Prenylation; Lipoprotein.
 FT NP_BIND 20 27 GTP (BY SIMILARITY).
 FT NP_BIND 67 71 GTP (BY SIMILARITY).
 FT NP_BIND 126 129 GTP (BY SIMILARITY).
 FT DOMAIN 42 50 EFFECTOR REGION (BY SIMILARITY).
 FT DOMAIN 185 191 POLY-LYS.

FT LIPID 205 205 GERANYL-GERANYL (BY SIMILARITY).
 SQ SEQUENCE 208 AA; 23887 MW; 0869627A12C67E8A CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKK 29
 185 KKKKK 190

Db 185 KKKKK 190

RESULT 37
 RISA BUCAI
 ID RISA BUCAI STANDARD; PRT; 208 AA.
 AC P57212;
 DT 16-OCT-2001 (Rel. 40, Created)
 DT 16-OCT-2001 (Rel. 40, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Riboflavin synthase alpha chain (EC 2.5.1.9).
 GN RIBE OR BU112
 OS Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
 symbiotic bacterium).
 OC Bacteria; Proteobacteria; gamma subdivision; Buchnera.
 OX NCBI_TaxID=118099;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Tokyo 1998.
 RX MEDLINE=20445173; PubMed=10993077;
 RA Shigenobu S, Watanabe H, Hattori M, Sakaki Y, Ishikawa H.;
 RT "Genome sequence of the endocellular bacterial symbiont of aphids
 Buchnera sp. APS";
 RL Nature 407:81-86(2000).
 CC -1- FUNCTION: RIBOFLAVIN SYNTHASE IS A BIFUNCTIONAL ENZYME COMPLEX
 CATALYZING THE FORMATION OF RIBOFLAVIN FROM 5-AMINO-6-(1'-D)-
 RIBITYL-AMINO-2,4(1H,3H)-PYRIMIDINEDIONE AND L-3,4-DIHYDROXY-2-
 BUTANONE-4-PHOSPHATE VIA 6,7-DIMETHYL-8-LUMAZINE. THE ALPHA
 SUBUNIT CATALYZES THE DISMUTATION OF 6,7-DIMETHYL-8-LUMAZINE TO
 RIBOFLAVIN AND 5-AMINO-6-(1'-D)-RIBITYL-AMINO-2,4(1H,3H)-
 PYRIMIDINEDIONE (BY SIMILARITY).
 CC -1- CATALYTIC ACTIVITY: 2,6,7-dimethyl-8-(1'-D-ribityl)lumazine -
 riboflavin + 4-(1'-D-ribitylamino)-5-amino-2,6-dihydroxypyrimidine.
 CC -1- PATHWAY: FINAL STEPS OF RIBOFLAVIN SYNTHESIS.
 CC -1- SUBUNIT: OLIGOMER THAT CONSIST OF 3 ALPHA SUBUNITS AND 60 BETA
 SUBUNITS (BY SIMILARITY).
 CC -1- SIMILARITY: TO BIOLUMINESCENCE ANTENNA PROTEINS LUXY (YFP) AND
 LUXL (LUMP).
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CC EMBL; AP001118; BAB12830.1; -
 CC InterPro: IPR001783; Lum_binding.
 DR Pfam: PF00677; Lum_binding; 2.
 DR ProDom: PD004110; Lum_binding; 2.
 DR TIGRFAMs: TIGR00187; ribe; 1.
 DR PROSITE: PS00693; LUM_BINDING; FALSE_NEG.
 KM Riboflavin biosynthesis; Transference; Repeat; Complete proteome.
 FT REPEAT 1 97
 FT REPEAT 98 201
 FT SITE 81 85 BINDS TO LUMAZINE (PROBABLE).
 FT SITE 179 183 BINDS TO LUMAZINE (PROBABLE).
 SQ SEQUENCE 208 AA; 23505 MW; 7CCE3272CF54BA5B CRC64;

Query Match
 Best Local Similarity 100.0%; Pred. No. 51;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;


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OY      23 EKKKKK 28
        |||||
Db       16 EKKKKK 21

RESULT 38
RHO1_YEAST      STANDARD:      PRT;      209 AA.
ID   RHO1_YEAST
AC   P06780;
DT   01-JAN-1988 (Rel. 06, Created)
DT   01-JAN-1988 (Rel. 06, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   RHO1 protein.
GN   RHO1 OR YPR165W OR P9325.3.
OS   Saccharomyces cerevisiae (Baker's Yeast).
OC   Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC   Saccharomycetiales; Saccharomycetaceae; Saccharomyces.
OX   NCBI_TaxId=4932;

RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=87118248; PubMed=3543936;
RA      Madule P., Axel R., Myers A.M.;
RT      "Characterization of two members of the rho gene family from the
RL      yeast Saccharomyces cerevisiae.";
RL      Proc. Natl. Acad. Sci. U.S.A. 84:779-783(1987).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      STRAIN=S288C / AB972;
RX      MEDLINE=97313271; PubMed=9169875;
RA      Bussey H., Storms R.K., Ahmed A., Albermann K., Allen E., Ansoerge W.,
RA      Aratijo R., Aparicio A., Barrell B.G., Badcock K., Benes V.,
RA      Botstein D., Bowman S., Bruckner M., Carpenter J., Cherry J.M.,
RA      Chung E., Churcher C.M., Coster F., Davis K., Davis R.W.,
RA      Dietrich F.S., Dillus H., DiPaolo T., Dubois E., Duesterhoeft A.,
RA      Duncan M., Fleetham M., Fortin N., Friesen J.D., Fritz C., Goffeau A.,
RA      Hall J., Hebling U., Heumann K., Hilbert H., Hillier L.,
RA      Hunnicke-Smith S., Hyman R., Johnston M., Kaiman S., Kleene K.,
RA      Komp C., Kurdl O., Lashkari D., Lew H., Lin A., Lin D., Louis E.J.,
RA      Marthe R., Messenguy F., Mewes H.-W., Miliptat S., Moestl D.,
RA      Mueller-Auer S., Namath A., Neutwich U., Oefner P., Pearson D.,
RA      Petel F.X., Pohl T.M., Purnelle D., Schafer M., Scharte M.,
RA      Scherens B., Schramm S., Schroeder M., Sidu A.M., Tettelin H.,
RA      Urrutiarazu L.A., Ushinsky S., Vierendeels F., Vissers S., Voss H.,
RA      Walsh S.V., Wambutt R., Wang Y., Wedler E., Wedler H., Winnelt E.,
RA      Zhong W.W., Zollner A., Vo D.H., Hani J.;
RT      "The nucleotide sequence of Saccharomyces cerevisiae chromosome XVI.";
RL      Nature 387:103-105(1997).
RN      [3]
RP      SEQUENCE OF 201-209 FROM N.A.
RX      MEDLINE=87137621; PubMed=3029111;
RA      Myers A.M., Crivellone M.D., Tzagoloff A.;
RT      "Assembly of the mitochondrial membrane system. MRP1 and MRP2, two
RT      yeast nuclear genes coding for mitochondrial ribosomal proteins.";
RL      J. Biol. Chem. 262:3388-3397(1987).
CC      -!- SIMILARITY: BELONGS TO THE SMALL GTPASE SUPERFAMILY. RHO FAMILY.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M15189; AAA34977.1; -
DR      EMBL: U25840; AAB68152.1; -
DR      EMBL: M15161; AAA4729.1; -
DR      PIR: A26587; TVBYH1.
DR      HSSP: P06749; 1FTN.
DR      SGD: S0006369; RHO1.
DR      InterPro: IPR003578; GTPase_Rho.
DR      InterPro: IPR001230; Prenyl_site.
DR      InterPro: IPR001806; Ras_transfmg.

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DR      InterPro: IPR005225; Small_GTP.
DR      Pfam: PF00071; ras. 1.
DR      PRINTS: PR00449; RASTRNSFRMNG.
DR      SMART: SM00174; RHO. 1.
DR      TIGRfams: TIGR00231; small_GTP. 1.
KW      GTP-binding; Prenylation; Lipoprotein.
FT      NP_BIND 17 24
FT      NP_BIND 64 68
FT      NP_BIND 122 125
FT      NP_BIND 39 47
FT      DOMAIN 206 206
FT      LIPID 206 206
SQ      SEQUENCE 209 AA; 23152 MW; 630B17E9E34CE75 CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 209;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      23 EKKKKK 28
        |||||
Db       200 EKKKKK 205

RESULT 39
T402_BURCE      STANDARD:      PRT;      211 AA.
ID   T402_BURCE
AC   P24536;
DT   01-MAR-1992 (Rel. 21, Created)
DT   01-MAR-1992 (Rel. 21, Last sequence update)
DT   15-JUN-2002 (Rel. 41, Last annotation update)
DE   Putative transposase for insertion sequence element IS402.
OC   Burkholderia cepacia (Pseudomonas cepacia).
OC   Bacteria; Proteobacteria; beta subdivision; Burkholderia group;
OC   Burkholderia.
OX   NCBI_TaxId=292;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=91323723; PubMed=1650732;
RA      Ferrante A.A., Lessie T.G.;
RT      "Nucleotide sequence of IS402 from Pseudomonas cepacia.";
RL      Gene 102:143-144(1991).
CC      -!- FUNCTION: INVOLVED IN THE TRANSPOSITION OF THE INSERTION
CC      SEQUENCE (BY SIMILARITY).
CC      -!- SIMILARITY: BELONGS TO THE TRANSPOSASE FAMILY 13.
CC      -----
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CC      or send an email to license@isb-sib.ch).
CC      -----
DR      EMBL: M64065; -, NOT_ANNOTATED_CDS.
DR      PIR: J01133; J01133.
DR      InterPro: IPR002559; Transposase_11.
DR      Pfam: PF01609; Transposase_11. 1.
KW      Hypothetical protein; Transposase element; Transposition;
KW      DNA-binding; DNA recombination.
SQ      SEQUENCE 211 AA; 23968 MW; ASDC96961EA820B CRC64;

Query Match
Best Local Similarity 100.0%; Score 6; DB 1; Length 211;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      4 GSLARA 9
        |||||
Db       21 GSLARA 26

RESULT 40
KSI_HYDAT
ID   KSI_HYDAT      STANDARD:      PRT;      217 AA.
AC   P38978;

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DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 01-OCT-1996 (Rel. 34, Last annotation update)
 DE KSI protein precursor (Head-specific protein 1) (Kopf-spezifisches protein 1).
 GN KSI.
 OS Hydra attenuata (Hydra) (Hydra vulgaris).
 OC Eukaryota; Metazoa; Cnidaria; Hydrozoa; Hydroida; Anthomedusae;
 CC Hydrozoa; Hydra.
 CC NCBI_TaxID=6087;
 RN [1]
 RP MEDLINE=95044930; PubMed=7956827;
 RA Weinzierl R., Salgado L.M., David C.N., Bosch T.C.G.;
 RT "Ksi, an epithelial cell-specific gene, responds to early signals of head formation in Hydra."
 RL Development 120:2511-2517(1994).
 CC -1- FUNCTION: RESPONDS TO EARLY SIGNALS OF HEAD FORMATION IN HYDRA.
 CC -1- TISSUE SPECIFICITY: EXPRESSED IN TENTACLE-SPECIFIC EPITHELIAL CELLS (BATTERY CELLS) AS WELL AS IN A SMALL FRACTION OF ECTODERMAL EPITHELIAL CELLS IN THE GASTRIC REGION SUBJACENT TO THE TENTACLES (THE TENTACLE FORMATION REGION). THE LATER CELLS ARE COMMITTED TO BECOME BATTERY CELLS.
 CC -1- INDUCTION: BY PKC.
 CC -----
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 CC -----
 DR EMBL: X78596; CA55331.1; -
 DR PIR: S43193; S43193.
 KW Developmental protein; Signal; Repeat.
 FT SIGNAL 1 16
 FT CHAIN 17 217
 FT DOMAIN 32 147
 FT REPEAT 32 81
 FT REPEAT 98 147
 FT DOMAIN 32 45
 FT DOMAIN 47 96
 FT DOMAIN 97 111
 FT DOMAIN 113 147
 FT DOMAIN 148 217
 SQ SEQUENCE 217 AA; 25427 MW; 0010423D1364B4B8 CRC64;
 Query Match 10.2%; Score 6; DB 1; Length 217;
 Best Local Similarity 100.0%; Pred. No. 52;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 EKKKKK 28
 DB 96 EKKKKK 101
 RESULT 41
 FLIZ_BACSU
 ID FLIZ_BACSU STANDARD; PRT; 219 AA.
 AC P35336;
 DT 01-JUN-1994 (Rel. 29, Created)
 DT 01-JUN-1994 (Rel. 29, Last sequence update)
 DT 15-JUN-2002 (Rel. 41, Last annotation update)
 DE Flagellar biosynthetic protein fliz precursor.
 GN FLIZ OR CHEA.
 OS Bacillus subtilis.
 OC Bacteria; Firmicutes; Bacillales; Bacillaceae; Bacillus.
 CC NCBI_TaxID=1423;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168 / O11085;
 RX MEDLINE=92283757; PubMed=1597417;

RA Bischoff D.S., Weinreich M.D., Ordel G.W.;
 RT "Nucleotide sequences of Bacillus subtilis flagellar biosynthetic genes fliz and fliz0 and identification of a novel flagellar gene, fliz1."
 RT fliz1.
 RL J. Bacteriol. 174:4017-4025(1992).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=168;
 RX MEDLINE=98044033; PubMed=9384377;
 RA Kunst F., Ogasawara N., Moszer I., Albertini A.M., Alloni G., Azevedo V., Bertero M.G., Bessieres P., Bolotin A., Borchert S., Borries R., Boursier L., Brans A., Braun M., Britnell S.C., Bron S., Brouillet S., Bruschi C.V., Caldwell B., Capuano V., Carter N.M., Choi S.K., Codani J.J., Conerton I.F., Cummings N.J., Daniel R.A., Denizot F., Devigne K.M., Dusterhoft A., Ehrlich S.D., Emmerson P.T., Enlian K.D., Errington J., Fabret C., Ferrari E., Foulger D., Fritz C., Fujita M., Fujita Y., Fuma S., Gallazzi A., Galleron N., Ghim S.Y., Glaser P., Goffeau A., Gollubly E.J., Grand G., Giuseppe G., Guy B.J., Haga K., Halech J., Harwood C.R., Henaut A., Hilbert H., Holsappel S., Hosono S., Hullo M.F., Itaya M., Jones L., Joris B., Karamata D., Kasahara Y., Klaert-Blanchard M., Klein C., Kobayashi Y., Koetter P., Koningsstein G., Krogh S., Kumano M., Kurita K., Lapidus A., Lardinois S., Lauber J., Lazarevic V., Lee S.M., Levine A., Liu H., Masuda S., Manuel C., Medigue C., Medina N., Mellado R.P., Mizuno M., Moestl D., Nakai S., Noback M., Noone D., O'Reilly M., Ogawa K., Ogiwara A., Oudega B., Park S.H., Parro V., Pohl T.M., Portetelle D., Portolillo S., Prescott A.M., Prescann E., Puig P., Purnelle B., Rapoport G., Rey M., Reynolds S., Rieger M., Rivolta C., Rocha E., Roche B., Rose M., Sadate Y., Sato T., Scanlan E., Schleich S., Schreier R., Scoffone F., Sekiguchi J., Sekowska A., Seror S.J., Seror P., Shin B.S., Soldo B., Sorokin A., Tacconi E., Takagi T., Takahashi H., Takemaru K., Takeuchi M., Tamakoshi A., Tanaka T., Terstra P., Tognoni A., Tosato V., Uchiyama S., Vandenbol M., Vamler F., Vassarotti A., Viari A., Wambuit R., Wedler E., Wedler H., Weitzsaecker T., Winters P., Wipat A., Yamamoto H., Yamane K., Yasumoto K., Yata K., Yoshida K., Yoshikawa H.F., Zumbstein E., Yoshikawa H., Danchin A.;
 RT "The complete genome sequence of the Gram-positive bacterium Bacillus subtilis".
 RL Nature 390:249-256(1997).
 CC -1- FUNCTION: MAY BE A STRUCTURAL COMPONENT OF THE FLAGELLUM THAT ANCHORS THE ROD TO THE MEMBRANE.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein (Potential).
 CC -----
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 CC -----
 DR EMBL: M87005; AAA22452.1; -
 DR EMBL: Z99112; CAB13507.1; -
 DR PIR: B41886; B41886.
 DR Subtilist; BG10259; fliz.
 KW Flagella; Signal; Transmembrane; Complete proteome.
 FT SIGNAL 1 26
 FT CHAIN 27 219
 FT TRANSMEM 71 96
 SQ SEQUENCE 219 AA; 24871 MW; 6FE82AF8E1DAE8E CRC64;
 Query Match 10.2%; Score 6; DB 1; Length 219;
 Best Local Similarity 100.0%; Pred. No. 53;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 50 GKRRKP 55
 DB 210 GKRRKP 215
 RESULT 42
 UNG_BUCAI

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ID  UNG_BUCAL          STANDARD:      PRT:      220 AA.
AC  P57280;
DT  16-OCT-2001 (Rel. 40, Created)
DT  16-OCT-2001 (Rel. 40, Last sequence update)
DE  16-OCT-2001 (Rel. 40, Last annotation update)
DE  Utracil-DNA glycosylase (EC 3.2.2.-) (UDG).
GN  UNG OR BU183.
OS  Buchnera aphidicola (subsp. Acyrthosiphon pisum) (Acyrthosiphon pisum
OS  symbiotic bacterium).
OC  Bacteria: Proteobacteria: gamma subdivision: Buchnera.
OX  NCBI_TaxID=118099;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=Tokyo 1998;
RC  MEDLINE=20445173; PubMed=10993077;
RT  Shigenobu S., Matanabe H., Hattori M., Sakaki Y., Ishikawa H.;
RT  "Genome sequence of the endocellular bacterial symbiont of aphids
RT  Buchnera sp. APS."
RL  Nature 407:81-86(2000).
CC  -1- FUNCTION: EXCISES URACIL RESIDUES FROM THE DNA WHICH CAN ARISE
CC  AS A RESULT OF MISINCORPORATION OF DUMP RESIDUES BY DNA
CC  POLYMERASE OR DUE TO DEAMINATION OF CYTOSINE (BY SIMILARITY).
CC  -1- SUBCELLULAR LOCATION: Cytoplasmic (By similarity).
CC  -1- SIMILARITY: BELONGS TO THE URACIL-DNA GLYCOSYLASE FAMILY.
CC  -----
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CC  -----
DR  EMBL: AF001118; BAB12900.1; -
DR  HSSP: P12295; 1EUG.
DR  InterPro: IPR005122; UDNA_glycos.
DR  InterPro: IPR002043; U_DNA_glycosylase.
DR  InterPro: IPR003249; U_glycosyl.
DR  Pfam: PF03167; UDG; 1.
DR  ProDom: PD001589; U_glycosyl. 1.
DR  TIGRFAMs: TIGR00628; ung; 1.
DR  PROSITE: PS00130; U_DNA_GLYCOSYLASE; 1.
KW  DNA repair; Hydrolase; Glycosidase; Complete proteome.
FT  ACT_SITE 61 61  GENERAL BASE (BY SIMILARITY).
SQ  SEQUENCE 220 AA; 25653 MW; AEAFL9BEE0A2942C CRC64;

Query Match          10.2%; Score 6; DB 1; Length 220;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  22 QEKKK 27
    |||||
DB  11 QEKKK 16

RESULT 43
RS3A_PYRAE          STANDARD:      PRT:      221 AA.
ID  RS3A_PYRAE
AC  O82721;
DT  15-JUN-2002 (Rel. 41, Created)
DT  15-JUN-2002 (Rel. 41, Last sequence update)
DT  15-JUN-2002 (Rel. 41, Last annotation update)
DE  30S ribosomal protein S3ae.
GN  RPS3AE OR PAE3472.
OS  Pyrobaculum aerophilum.
OC  Archaea: Crenarchaeota: Thermoprotei; Thermoproteales;
OC  Thermoproteaceae; Pyrobaculum.
OX  NCBI_TaxID=13773;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=IM2 / ATCC 51768 / DSM 7523;
RC  PubMed=11792869;
RA  Fitz-Gibbon S.T., Ladner H., Kim U.-J., Stetter K.O., Simon M.I.,

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RA  Miller J.H.;
RT  "Genome sequence of the hyperthermophilic crenarchaeon Pyrobaculum
RT  aerophilum.";
RL  Proc. Natl. Acad. Sci. U.S.A. 99:984-989(2002).
CC  -1- SIMILARITY: BELONGS TO THE S3AE FAMILY OR RIBOSOMAL PROTEINS.
CC  -----
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CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: AE009933; AAL64942.1; -
DR  InterPro: IPR001593; Ribosomal_S3AE.
DR  Pfam: PF01015; Ribosomal_S3AE; 1.
DR  ProDom: PD003035; Ribosomal_S3AE; 1.
DR  PROSITE: PS01191; RIBOSOMAL_S3AE; FALSE_NEG.
KW  Ribosomal protein; Complete proteome.
SQ  SEQUENCE 221 AA; 24761 MW; 19F91730136136AA CRC64;

Query Match          10.2%; Score 6; DB 1; Length 221;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY  19 VAKOEK 24
    |||||
DB  8 VAKOEK 13

RESULT 44
YJ08_YEAST          STANDARD:      PRT:      233 AA.
ID  YJ08_YEAST
AC  P47006;
DT  01-FEB-1996 (Rel. 33, Created)
DT  01-FEB-1996 (Rel. 33, Last sequence update)
DT  01-OCT-1996 (Rel. 34, Last annotation update)
DE  Hypothetical 26.9 kDa protein in INO1-ID52 intergenic region.
GN  YJ148W OR J0637.
OS  Saccharomyces cerevisiae (Baker's yeast).
OC  Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
OC  Saccharomycetales; Saccharomycetaceae; Saccharomyces.
OX  NCBI_TaxID=4932;
RN  [1]
RP  SEQUENCE FROM N.A.
RC  STRAIN=S288c / FY1679;
RC  MEDLINE=96408771; PubMed=8813765;
RA  Katsoulou C., Tzeremia M., Tavernarakis N., Alexandraki D.;
RT  "Sequence analysis of a 40.7 kb segment from the left arm of yeast
RT  chromosome X reveals 14 known genes and 13 new open reading frames
RT  including homologues of genes clustered on the right arm of
RT  chromosome XI."
RL  Yeast 12:787-797(1996).
CC  -----
CC  This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC  the European Bioinformatics Institute. There are no restrictions on its
CC  use by non-profit institutions as long as its content is in no way
CC  modified and this statement is not removed. Usage by and for commercial
CC  entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC  or send an email to license@isb-sib.ch).
CC  -----
DR  EMBL: Z49423; CAA89443.1; -
DR  SCD: X87371; CAA80807.1; -
DR  SGD: S0003684; YJL148W.
KW  Hypothetical protein.
FT  DOMAIN 184 233  GLU/LYS-RICH.
FT  DOMAIN 208 215  POLY-LYS.
FT  DOMAIN 221 230  POLY-LYS.
SQ  SEQUENCE 233 AA; 26875 MW; DCD42DEC374EDB6 CRC64;

Query Match          10.2%; Score 6; DB 1; Length 233;

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Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: February 6, 2003, 21:31:12
Job time : 14 secs

OY 23 EKKKK 28
DB 207 EKKKK 212

RESULT 45

CAVL_CAEEL STANDARD; PRT; 235 AA.
AC Q94051;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE Caveolin-1.
GN CAV-1 OR T13F2.8.
OS Caenorhabditis elegans.
OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC Rhabditidae; Peloderinae; Caenorhabditis.
OX NCBI_TaxID=6239;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RX MEDLINE=97153022; PubMed=8999956;
RA Tang Z., Okamoto T., Boontarakulpoontawe P., Katada T., Otsuka A.J.,
RA Lisanti M.P.;
RT "Identification, sequence, and expression of an invertebrate caveolin
RT gene family from the nematode Caenorhabditis elegans. Implications
RT for the molecular evolution of mammalian caveolin genes.";
RL J. Biol. Chem. 272:2437-2445(1997).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-Bristol N2;
RA Swindburne J.;
RL Submitted (NOV-1996) to the EMBL/Genbank/DBJ databases.
CC -1- FUNCTION: MAY ACT AS A SCAFFOLDING PROTEIN WITHIN CAVEOLAR
CC MEMBRANES. INTERACTS DIRECTLY WITH G-PROTEIN ALPHA SUBUNITS AND
CC CAN FUNCTIONALLY REGULATE THEIR ACTIVITY.
CC -1- SUBUNIT: HOMODIMER CONTAINING 14-16 MONOMERS PER OLIGOMER.
CC -1- SUBCELLULAR LOCATION: MEMBRANE PROTEIN OF CAVEOLAE. POTENTIAL
CC HAIRPIN-LIKE STRUCTURE IN THE MEMBRANE (BY SIMILARITY).
CC -1- SIMILARITY: BELONGS TO THE CAVEOLIN FAMILY.
CC
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
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CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
CC or send an email to license@isb-sib.ch).
CC
CC
CC EMBL: U66405; AAB48388.1; -
CC EMBL: Z81122; CAB03359.1; -
CC WormPep: T13F2.8; CEL3633.
CC InterPro: IPR001612; Caveolin.
CC Pfam: PF01146; Caveolin.1.
CC PROSITE: PS01210; CAVEOLIN; FALSE_NEG.
KW Transmembrane; Lipoprotein; Palmitate.
FT DOMAIN 1 161 CYTOPLASMIC (POTENTIAL).
FT TRANSMEM 162 182 POTENTIAL.
FT DOMAIN 183 235 CYTOPLASMIC (POTENTIAL).
FT LIPID 234 234 PALMITATE (POTENTIAL).
SQ SEQUENCE 235 AA: 26291 MW; F07B12DEB4D6F13A CRC64;

Query Match 10.2%; Score 6; DB 1; Length 235;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 TFGKK 53
DB 46 TFGKK 51


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; PRIOR FILING DATE: EARLIER FILING DATE: 1997-08-18
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,785
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,664
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,660
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; PRIOR APPLICATION NUMBER: EARLIER APPLICATION NUMBER: 60/058,661
; PRIOR FILING DATE: EARLIER FILING DATE: 1997-09-12
; NUMBER OF SEQ ID NOS: 672
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 479
; LENGTH: 51
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-802-479

Query Match          10.2%: Score 6; DB 9; Length 51;
Best Local Similarity 100.0%; Pred. No. 28;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
    |||||
Db 35 EKKKKK 40

RESULT 24
US-09-764-869-1228
; Sequence 1228, Application US/09764869
; Patent No. US20020061521A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC007
; CURRENT APPLICATION NUMBER: US/09/764,869
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2442
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1228
; LENGTH: 52
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-869-1228

Query Match          10.2%: Score 6; DB 10; Length 52;
Best Local Similarity 100.0%; Pred. No. 29;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKK 29
    |||||
Db 9 KKKKKK 14

RESULT 25
US-09-764-855-113
; Sequence 113, Application US/09764855
; Patent No. US20020119919A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: P110
; CURRENT APPLICATION NUMBER: US/09/764,855
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 334
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 113
; LENGTH: 55
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
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; LOCATION: (19)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (36)
; OTHER INFORMATION: xaa equals any of the naturally occurring L-amino acids
US-09-764-855-113

Query Match          10.2%: Score 6; DB 10; Length 55;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
    |||||
Db 48 EKKKKK 53

RESULT 26
US-09-764-847-601
; Sequence 601, Application US/09764847
; Patent No. US20020132767A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC009
; CURRENT APPLICATION NUMBER: US/09/764,847
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 2003
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 601
; LENGTH: 56
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-847-601

Query Match          10.2%: Score 6; DB 10; Length 56;
Best Local Similarity 100.0%; Pred. No. 30;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
    |||||
Db 45 EKKKKK 50

RESULT 27
US-09-864-761-47593
; Sequence 47593, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL F
; FILE REFERENCE: Aeonlca-x-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47593
; LENGTH: 57
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AL049694.9
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.72
; OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.85
; OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.9
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 8.6
; OTHER INFORMATION: EXPRESSED IN HB100, SIGNAL = 0.88
; OTHER INFORMATION: SWISSPROT HIT: P1386, EVALU 5.00e-14
; OTHER INFORMATION: EST_HUMAN HIT: BF344101.1, EVALU 8.00e-18
; US-09-864-761-47593

Query Match          10.2%; Score 6; DB 10; Length 57;
Best Local Similarity 100.0%; Pred. No. 31;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      13 RCGTPK 18
        |||||
Db       6 RCGTPK 11

RESULT 28
; US-09-864-761-47812
; Sequence 47812, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
; FILE REFERENCE: Aemtica-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
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; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 47812
; LENGTH: 59
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC010290.4
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.51
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.5
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.64
; OTHER INFORMATION: EST_HUMAN HIT: BE244981.1, EVALU 1.00e-12
; US-09-864-761-47812

Query Match          10.2%; Score 6; DB 10; Length 59;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      23 EKKKK 28
        |||||
Db       16 EKKKK 21

RESULT 29
; US-09-989-919-118
; Sequence 118, Application US/09989919
; Patent No. US20020164344A1
; GENERAL INFORMATION:
; APPLICANT: Macina, Roberto
; APPLICANT: Recipon, Heve
; APPLICANT: Pluta, Jason
; APPLICANT: Ghosh, Malavika
; APPLICANT: Sun, Yongming
; APPLICANT: Liu, Chenghua
; TITLE OF INVENTION: Compositions and Methods Relating to Colon Specific Genes and
; FILE REFERENCE: DEX-0289
; CURRENT APPLICATION NUMBER: US/09/989,919
; CURRENT FILING DATE: 2001-11-21
; PRIOR APPLICATION NUMBER: 60/252,505
; PRIOR FILING DATE: 2000-11-22
; PRIOR APPLICATION NUMBER: 60/252,505
; NUMBER OF SEQ ID NOS: 124
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 118
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-989-919-118
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Query Match 10.2% Score 6; DB 9; Length 60;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||

DB 54 EKKKK 59

RESULT 30
US-09-925-300-1198
; Sequence 1198, Application US/09925300
; Patent No. US20020151681A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; APPLICANT: Steve Ruben,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1198
; LENGTH: 60
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-925-300-1198

Query Match 10.2% Score 6; DB 10; Length 60;
Best Local Similarity 100.0%; Pred. No. 32;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||

DB 53 EKKKK 58

RESULT 31
US-09-925-301-1475
; Sequence 1475, Application US/09925301
; Patent No. US20020052308A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA106
; CURRENT APPLICATION NUMBER: US/09/925,301
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05882
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1694
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1475
; LENGTH: 62
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (3)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (5)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (8)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (9)

OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (48)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (59)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-301-1475

Query Match 10.2% Score 6; DB 10; Length 62;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||

DB 36 EKKKK 41

RESULT 32
US-10-117-604-2
; Sequence 2, Application US/10117604
; Patent No. US20020168672A1
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING
; SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERE
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSER: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentln Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/117,604
; FILING DATE: 04-Apr-2002
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,089
; FILING DATE: <Unknown>
; APPLICATION NUMBER: US 60/030,987
; FILING DATE: 15-Nov-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P-CE 2862
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-10-117-604-2

Query Match 10.2% Score 6; DB 9; Length 63;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28

Db 15 EKKKKK 20

RESULT 33

US-09-764-846-260
; Sequence 260, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 260
; LENGTH: 63
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-260

Query Match 10.2%; Score 6; DB 10; Length 63;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
Db 25 EKKKKK 30

RESULT 34

US-09-864-761-45501
; Sequence 45501, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
; APPLICANT: Penn, Sharon G.
; APPLICANT: Rank, David R.
; APPLICANT: Hanzel, David K.
; APPLICANT: Chen, Wensheng
; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
; FILE REFERENCE: Aecm1ca-X-1
; CURRENT APPLICATION NUMBER: US/09/864,761
; CURRENT FILING DATE: 2001-05-23
; Prior application data removed - consult PALM or file wrapper
; PRIOR APPLICATION NUMBER: US 60/180,312
; PRIOR FILING DATE: 2000-02-04
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 09/632,366
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: GB 24263.6
; PRIOR FILING DATE: 2000-10-04
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: PCT/US01/00666
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00667
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00664
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00669
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00665
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00668
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00663
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00662
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00661

; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: PCT/US01/00670
; PRIOR FILING DATE: 2001-01-30
; PRIOR APPLICATION NUMBER: US 60/234,687
; PRIOR FILING DATE: 2000-09-21
; PRIOR APPLICATION NUMBER: US 09/608,408
; PRIOR FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: US 09/774,203
; PRIOR FILING DATE: 2001-01-29
; NUMBER OF SEQ ID NOS: 49117
; SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
; SEQ ID NO 45501
; LENGTH: 64
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: MAP TO AC008739.5
; OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 0.56
; OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.58
; OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.78
; OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 0.69
; OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.77
US-09-864-761-45501

Query Match 10.2%; Score 6; DB 10; Length 64;
Best Local Similarity 100.0%; Pred. No. 34;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
Db 51 EKKKKK 56

RESULT 35

US-09-764-846-224
; Sequence 224, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 224
; LENGTH: 66
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-224

Query Match 10.2%; Score 6; DB 10; Length 66;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
Db 39 EKKKKK 44

RESULT 36

US-09-764-877-1089
; Sequence 1089, Application US/09764877
; Patent No. US20020147140A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PC005
; CURRENT APPLICATION NUMBER: US/09/764,877
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - refer to PALM or file wrapper
; NUMBER OF SEQ ID NOS: 4031

SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1089
LENGTH: 66
TYPE: PRT
ORGANISM: Homo sapiens
US-09-764-877-1089

Query Match 10.2%; Score 6; DB 10; Length 66;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
|||||
DB 56: KKKKKT 61

RESULT 37
US-09-867-550-284
Sequence 284, Application US/09867550
Patent No. US20020082206A1
GENERAL INFORMATION:

APPLICANT: Leach, Martin D.
APPLICANT: Mehraban, Fuad,
APPLICANT: Conley, Pamela
APPLICANT: Law, Debbie
APPLICANT: Topper, James
TITLE OF INVENTION: No. US20020082206A1el Polynucleotides from Atherogenic Cells and
FILE REFERENCE: 21402-013 (Cura-313)
CURRENT APPLICATION NUMBER: US/09/867,550
CURRENT FILING DATE: 2001-09-20
PRIOR APPLICATION NUMBER: USSN 60/208,427
PRIOR FILING DATE: 2000-05-30
NUMBER OF SEQ ID NOS: 2125
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 284
LENGTH: 67
TYPE: PRT
ORGANISM: Homo sapiens
US-09-867-550-284

Query Match 10.2%; Score 6; DB 10; Length 67;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKKK 53
|||||
DB 28 TFGKKK 33

RESULT 38
US-09-201-936-18
Sequence 18, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:
APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 18
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-18

Query Match 10.2%; Score 6; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10
|||||
DB 21 SLARAG 26

RESULT 39
US-09-201-936-19
Sequence 19, Application US/09201936
Publication No. US20020187946A1
GENERAL INFORMATION:

APPLICANT: Korneluk, Robert G.
APPLICANT: Mackenzie, Alexander E.
APPLICANT: Baird, Stephen
APPLICANT: Liston, Peter
TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
TITLE OF INVENTION: PROBES, AND DETECTION METHODS
FILE REFERENCE: 07891/003003
CURRENT APPLICATION NUMBER: US/09/201,936
CURRENT FILING DATE: 1998-12-01
EARLIER APPLICATION NUMBER: 09/011,356
EARLIER FILING DATE: 1998-02-04
EARLIER APPLICATION NUMBER: PCT/IB96/01022
EARLIER FILING DATE: 1996-08-05
EARLIER APPLICATION NUMBER: 08/576,956
EARLIER FILING DATE: 1995-12-22
EARLIER APPLICATION NUMBER: 08/511,485
EARLIER FILING DATE: 1995-08-04
NUMBER OF SEQ ID NOS: 45
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 19
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
US-09-201-936-19

Query Match 10.2%; Score 6; DB 9; Length 68;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10
|||||
DB 21 SLARAG 26

RESULT 40
US-09-764-846-191
Sequence 191, Application US/09764846
Patent No. US20020102638A1
GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
FILE REFERENCE: PT212
CURRENT APPLICATION NUMBER: US/09/764,846
CURRENT FILING DATE: 2001-01-17
Prior application data removed - consult PALM or file wrapper
NUMBER OF SEQ ID NOS: 348
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 191
LENGTH: 68
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:

```
; NAME/KEY: SITE
; LOCATION: (66)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-764-846-191
```

```
Query Match          10.2%; Score 6; DB 10; Length 68;
Best Local Similarity 100.0%; Pred. No. 35;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 37 EKKKKK 42
```

RESULT 41

```
US-09-925-299-1340
; Sequence 1340, Application US/09925299
; Patent No. US20020055627A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA102
; CURRENT APPLICATION NUMBER: US/09/925,299
; PRIOR FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05883
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1556
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1340
; LENGTH: 69
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (9)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (60)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (67)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-299-1340
```

```
Query Match          10.2%; Score 6; DB 10; Length 69;
Best Local Similarity 100.0%; Pred. No. 36;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 19 EKKKKK 24
```

RESULT 42

```
US-09-764-846-179
; Sequence 179, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
```

```
; CURRENT FILING DATE: 2001-01-17
; APPLICATION DATA removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 179
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-179
```

```
Query Match          10.2%; Score 6; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 53 EKKKKK 58
```

RESULT 43

```
US-09-925-300-1105
; Sequence 1105, Application US/09925300
; Patent No. US2002015181A1
; GENERAL INFORMATION:
; APPLICANT: Craig Rosen,
; TITLE OF INVENTION: Nucleic Acids, Proteins and Antibodies
; FILE REFERENCE: PA101
; CURRENT APPLICATION NUMBER: US/09/925,300
; CURRENT FILING DATE: 2001-08-10
; PRIOR APPLICATION NUMBER: PCT/US00/05988
; PRIOR FILING DATE: 2000-03-08
; PRIOR APPLICATION NUMBER: 60/124,270
; PRIOR FILING DATE: 1999-03-12
; NUMBER OF SEQ ID NOS: 1890
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 1105
; LENGTH: 72
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: SITE
; LOCATION: (65)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
; NAME/KEY: SITE
; LOCATION: (69)
; OTHER INFORMATION: Xaa equals any of the naturally occurring L-amino acids
US-09-925-300-1105
```

```
Query Match          10.2%; Score 6; DB 10; Length 72;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
Oy 23 EKKKKK 28
    |||||
Db 55 EKKKKK 60
```

RESULT 44

```
US-09-764-846-242
; Sequence 242, Application US/09764846
; Patent No. US20020102638A1
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: Nucleic Acids, Proteins, and Antibodies
; FILE REFERENCE: PT212
; CURRENT APPLICATION NUMBER: US/09/764,846
; CURRENT FILING DATE: 2001-01-17
; Prior application data removed - consult PALM or file wrapper
; NUMBER OF SEQ ID NOS: 348
; SOFTWARE: Patentln Ver. 2.0
; SEQ ID NO 242
; LENGTH: 73
```

; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-764-846-242

Query Match 10.2%; Score 6; DB 10; Length 73;
Best Local Similarity 100.0%; Pred. No. 37;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28
|||||
DB 40 EKKKKK 45

RESULT 45
US-09-833-067-9
; Sequence 9, Application US/09833067
; Patent No. US2002005488A1
; GENERAL INFORMATION:
; APPLICANT: O'HANLEY, PETER
; APPLICANT: DENICH, KENNETH
; TITLE OF INVENTION: DISSOCIATED PILL, THEIR PRODUCTION AND USE
; FILE REFERENCE: 050939/0102
; CURRENT APPLICATION NUMBER: US/09/833,067
; CURRENT FILING DATE: 2001-04-12
; PRIOR APPLICATION NUMBER: 60/196,493
; PRIOR FILING DATE: 2000-04-12
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentl Ver. 2.1
; SEQ ID NO 9
; LENGTH: 75
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Amino acid
; OTHER INFORMATION: sequence of papH gene deletion mutant
US-09-833-067-9

Query Match 10.2%; Score 6; DB 10; Length 75;
Best Local Similarity 100.0%; Pred. No. 38;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 ARAGKV 12
|||||
DB 26 ARAGKV 31

Search completed: February 6, 2003, 21:32:50
Job time : 12 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 21:30:34 ; Search time 18 Seconds
(without alignments)
315.107 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KVGSLARAGKVRGQTPKVA.....RRFVNVVPTFGKKKGPNNNS 59

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 283224 seqs, 96134422 residues

Word size : 0

Total number of hits satisfying chosen parameters: 283224

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : PIR_73:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	59	100.0	133	1 A47416	ubiquitin-like pro
2	59	100.0	133	2 JC1278	ubiquitin-like pro
3	59	100.0	133	2 I48346	ribosomal protein
4	22	37.3	62	2 H85342	RIBOSOMAL PROTEIN
5	22	37.3	68	2 F84580	40S ribosomal prot
6	20	33.9	229	2 S38383	SEB4B protein - hu
7	13	22.0	130	2 T15642	hypothetical prote
8	12	20.3	58	2 A71604	ribosomal protein
9	12	20.3	61	2 T39834	ribosomal protein
10	12	20.3	63	1 S67074	ribosomal protein
11	8	13.6	135	2 A97094	uncharacterized pr
12	7	11.9	134	2 S02776	DNA-binding protei
13	7	11.9	154	2 B75305	hypothetical prote
14	7	11.9	199	2 E84782	probable homeodoma
15	7	11.9	215	2 I52523	nucleoporin p52 ho
16	7	11.9	233	2 H86318	probable 60S ribos
17	7	11.9	233	2 D96768	protein 60S riboso
18	7	11.9	233	2 E96768	protein 60S riboso
19	7	11.9	283	2 T47174	hypothetical prote
20	7	11.9	314	2 D70313	riboflavin kinase
21	7	11.9	346	2 T19629	hypothetical prote
22	7	11.9	424	2 T36154	probable ABC-type
23	7	11.9	454	2 E84153	replicative DNA he
24	7	11.9	710	2 T49516	Atu related protei
25	7	11.9	863	2 F85343	hypothetical prote
26	7	11.9	1254	1 J031979	structural polypor
27	7	11.9	2539	2 B71619	hypothetical prote
28	6	10.2	46	2 T28799	hypothetical prote
29	6	10.2	67	2 B69830	hypothetical prote

30	6	10.2	70	2 H97135	uncharacterized ph
31	6	10.2	74	2 T47434	hypothetical prote
32	6	10.2	80	2 B82267	exodeoxyribonuclea
33	6	10.2	81	2 S66013	ribosomal protein
34	6	10.2	92	2 T36134	hypothetical prote
35	6	10.2	92	2 H82867	transcription regu
36	6	10.2	98	2 H96585	hypothetical prote
37	6	10.2	102	2 T07078	cold stress protei
38	6	10.2	104	2 C87604	virulence-associat
39	6	10.2	105	2 PM0017	hypothetical prote
40	6	10.2	105	2 PM0018	hypothetical prote
41	6	10.2	106	2 S59536	cold stress protei
42	6	10.2	115	2 S69849	hypothetical prote
43	6	10.2	117	2 H84651	hypothetical prote
44	6	10.2	123	2 B71268	probable ribosomal
45	6	10.2	125	1 R3RT25	ribosomal protein

ALIGNMENTS

```
RESULT 1
A47416
ubiquitin-like protein / ribosomal protein S30, cytosolic [validated] - rat
N:Contains: ribosomal protein S30; ubiquitin-like protein
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jul-2000 #sequence_revision 21-Jul-2000 #text_change 21-Jul-2000
C:Accession: A47416; B47416; S18101
R:Olvera, J.; Wool, I.G.
J. Biol. Chem. 268, 17967-17974, 1993
A>Title: The carboxyl extension of a ubiquitin-like protein is rat ribosomal protein
A:Reference number: A47416; MUID:93352612; PMID:8394356
A:Accession: A47416
A:Molecule type: mRNA
A:Residues: 1-133 <OLV>
A:Cross-references: EMBL:X62671; NID:g407165; PIDN:CAA44545.1; PID:g57566
A:Accession: B47416
A:Molecule type: protein
A:Residues: 75-92 <OL2>
A>Note: the proteins are designated as ubiquitin-like protein and ribosomal protein &
C:Keywords: protein biosynthesis; ribosome
F:1-74/Product: ubiquitin-like protein #status predicted <UBI>
F:75-133/Product: ribosomal protein S30 #status experimental <RIB>

Query Match      100.0%; Score 59; DB 1; Length 133;
Best Local Similarity 100.0%; Pred. No. 5, 2e-52;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGQTPKVAKKKKTKGRARRRQYNNRFVNVVPTFGKKKGPNNNS 59
DB 75 KVGSLARAGKVRGQTPKVAKKKKTKGRARRRQYNNRFVNVVPTFGKKKGPNNNS 133

RESULT 2
JC1278
ubiquitin-like protein / ribosomal protein S30, cytosolic - human
N:Alternate names: fau protein
C:Species: Homo sapiens (man)
C>Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 24-Sep-1999
C:Accession: JC1278; I37387; S68911; S21449; S21450
R:Kas, K.; Michiels, L.; Merregaert, J.
Biochem. Biophys. Res. Commun. 187, 927-933, 1992
A>Title: Genomic structure and expression of the human fau gene: Encoding the ribosomal
A:Reference number: JC1278; MUID:92412144; PMID:1326960
A:Accession: JC1278
A:Molecule type: DNA
A:Residues: 1-113 <KAS>
A:Cross-references: EMBL:X65921; NID:g31304; PIDN:CAA46714.1; PID:g31305
R:Michiels, L.; Van der Raaij-MacLeod, E.; Van Hasselt, F.; Kas, K.; Merregaert, J.
Oncogene 8, 2537-2546, 1993
A>Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an
```

A:Reference number: I37387; MUID:93368957; PMID:8395683
A:Accession: I37387
A:Status: translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:X65923; NID:g31302; PIDN:CAA46716.1; PID:g31303
R.Vladimirov, S.N.; Ivanov, A.V.; Karпова, G.G.; Musolyamov, A.K.; Egorov, T.A.; Thiede, R.J. Biochem. 239, 144-149, 1996
A:Title: Characterization of the human small-ribosomal-subunit proteins by N-terminal an
A:Reference number: S68911; MUID:96305378; PMID:8706699
A:Accession: S68911
A:Molecule type: protein
A:Residues: 75-99 <VLA>
C:Genetics:
A:Gene: fau
A:Introns: 25/3; 74/1; 92/3
C:Superfamily: unassigned ubiquitin-related proteins: ubiquitin homology
C:Keywords: protein biosynthesis; ribosome
F:1-74/Domain: ubiquitin homology <UBH>
F:75-133/Product: ribosomal protein S30, cytosolic #status experimental <MAT>

Query Match 100.0%; Score 59; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKVAKOEKKKKTKGRARRRQYRRFVNVPTFGKKGPAN 59
DB 75 KVGSLARAGKVRGOTPKVAKOEKKKKTKGRARRRQYRRFVNVPTFGKKGPAN 133

RESULT 3
148346
ribosomal protein fau - mouse
N:Alternate names: gene fau protein; monoclonal nonspecific suppressor factor beta
C:Species: Mus musculus (house mouse)
C:Date: 12-Aug-1996 #sequence_revision 12-Aug-1996 #text_change 24-Sep-1999
C:Accession: I48346; A56532; I59368; S21452
R.Michiels, L.; Van der Raueelaert, E.; Van Hasselt, F.; Kas, K.; Merregaert, J.
Oncogene 8, 2537-2546, 1993
A:Title: fau cDNA encodes a ubiquitin-like-S30 fusion protein and is expressed as an ant
A:Reference number: I37387; MUID:93368957; PMID:8395683
A:Accession: I48346
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RES>
A:Cross-references: EMBL:X65922; NID:g50949; PIDN:CAA46715.1; PID:g50950
R.Castels, D.; Poitrier, C.; Guenet, J.L.; Merregaert, J.
Genomics 25, 291-294, 1995
A:Title: The mouse fau gene: genomic structure, chromosomal localization, and characteri
A:Reference number: A56532; MUID:95293388; PMID:7774934
A:Accession: A56532
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-133 <CAS>
A:Cross-references: GB:I33715; NID:g497610; PIDN:AA91564.1; PID:g497611
A:Note: authors translated the codon GTT for residue 119 as Atg, and GTC for residue 120
Proc. Natl. Acad. Sci. U.S.A. 92, 3463-3467, 1995
A:Title: Molecular cloning and characterization of a cDNA encoding monoclonal nonspecific
A:Reference number: I59368; MUID:95241522; PMID:7724584
A:Accession: I59368
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-133 <RE2>
A:Cross-references: GB:D26610; NID:g1060926; PIDN:BAA05655.1; PID:g1060927
C:Genetics:
A:Gene: fau
A:Introns: 25/3; 74/1; 92/3
C:Superfamily: unassigned ubiquitin-related proteins: ubiquitin homology
F:1-74/Domain: ubiquitin homology <UBH>

Query Match 100.0%; Score 59; DB 2; Length 133;
Best Local Similarity 100.0%; Pred. No. 5.2e-52;

Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKVAKOEKKKKTKGRARRRQYRRFVNVPTFGKKGPAN 59
DB 75 KVGSLARAGKVRGOTPKVAKOEKKKKTKGRARRRQYRRFVNVPTFGKKGPAN 133

RESULT 4
H85342
RIBOSOMAL PROTEIN S30 homolog (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 16-Feb-2001
C:Accession: H85342
R.anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Sp
Nature 402, 769-777, 1999
A:Title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Accession: H85342
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-62 <STO>
A:Cross-references: GB:NC_001268; NID:g7269837; PIDN:CAB79697.1; GSPDB:GN00140
C:Genetics:
A:Gene: AT4g29390
A:Map position: 4

Query Match 37.3%; Score 22; DB 2; Length 62;
Best Local Similarity 100.0%; Pred. No. 4.3e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKVAKQ 22
DB 3 KVGSLARAGKVRGOTPKVAKQ 24

RESULT 5
P84580
40S ribosomal protein S30 (imported) - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 17-May-2002
C:Accession: P84580
R.Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vankken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: A84420; MUID:20083487; PMID:10617197
A:Accession: P84580
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-68 <STO>
A:Cross-references: GB:AE002093; NID:g3687243; PIDN:AAC62141.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g19750
A:Map position: 2
C:Superfamily: yeast ribosomal protein S30.e

Query Match 37.3%; Score 22; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 4.7e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVRGOTPKVAKQ 22
DB 9 KVGSLARAGKVRGOTPKVAKQ 30

RESULT 6
S38383
SPB4B protein - human (fragment)
C:Species: Homo sapiens (man)
C:Date: 06-Feb-1995 #sequence_revision 06-Feb-1995 #text_change 08-Sep-1997
C:Accession: S38383
R.Ruehlmann, A.; Gupta, A.; Terworst, C.

submitted to the EMBL Data Library, September 1993
A:Description: A novel murine RRM-type protein and its human homolog.

A:Reference number: S38382

A:Accession: S38383

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-229 <RUE>

A:Cross-references: EMBL:X75315

C:Superfamily: unassigned ribonucleoprotein repeat-containing proteins; ribonucleoprotein repeat homology <RRM1>
F:25-91/Domain: ribonucleoprotein repeat homology <RRM1>

Query Match

Best Local Similarity 33.9%; Score 20; DB 2; Length 229;
Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 35 RMQYRRRVNVPFGKKKG 54

Db 1 RMQYRRRVNVPFGKKKG 20

RESULT 7

hypothetical protein C26F1.4 - *Caenorhabditis elegans*

C:Species: *Caenorhabditis elegans*

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 24-Nov-1999

C:Accession: T15642

R:Geisel, C.; Stellyes, L.; Bradshaw, H.

submitted to the EMBL Data Library, March 1996

A:Description: The sequence of *C. elegans* cosmid C26F1.

A:Reference number: Z18381

A:Accession: T15642

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-130 <GEI>

A:Cross-references: EMBL:U53148; NID:g1255375; PID:g1255381; PIDN:AAB37076.1; GSPDB:GN0C

A:Experimental source: strain Bristol NZ; clone C26F1

C:Genetics:

A:Gene: CESP:C26F1.4

A:Map position: 5

A:Introns: 27/3; 71/1

C:Superfamily: unassigned ubiquitin-related proteins; ubiquitin homology

Query Match

Best Local Similarity 22.0%; Score 13; DB 2; Length 130;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSRLARAKVR 13

Db 72 KVHGSRLARAKVR 84

RESULT 8

ribosomal protein S30 PRB0885w - malaria parasite (*Plasmodium falciparum*)

C:Species: *Plasmodium falciparum*

C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 13-Aug-1999

C:Accession: A71604

R:Gardner, M.J.; Tettein, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.V.;

; Ferreira, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H.O.

Science 282, 1126-1132, 1998

A:Title: Chromosome 2 sequence of the human malaria parasite *Plasmodium falciparum*.

A:Reference number: A71600; MUID:99021743; PMID:9804551

A:Accession: A71604

A>Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-58 <GAR>

A:Cross-references: GB:AE001422; GB:AE001362; NID:g3845298; PIDN:AAC71966.1; PID:g384530

A:Experimental source: clone 3D7

C:Genetics:

A:Gene: PRB0885w

C:Superfamily: yeast ribosomal protein S30.e

Query Match

20.3%; Score 12; DB 2; Length 58;

Best Local Similarity 100.0%; Pred. No. 4.6e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSRLARAKVR 12

Db 3 KVHGSRLARAKVR 14

RESULT 9

ribosomal protein s30 - fission yeast (*Schizosaccharomyces pombe*)

C:Species: *Schizosaccharomyces pombe*

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 02-Jun-2000

C:Accession: T39834

R:Lyne, M.; Rajandream, M.A.; Barrell, B.G.; Devlin, K.; Churcher, C.M.

submitted to the EMBL Data Library, February 1998

A:Reference number: Z21884

A:Accession: T39834

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-61 <LYN>

A:Cross-references: EMBL:AL021839; PIDN:CAA17057.2; GSPDB:GN00067; SPDB:SPBC1967.03c

A:Experimental source: strain 972h-; cosmid c1967

C:Genetics:

A:Gene: SPDB:SPBC1967.03c

A:Map position: 2

A:Introns: 13/3; 56/3

C:Superfamily: yeast ribosomal protein S30.e

Query Match

Best Local Similarity 100.0%; Pred. No. 4.8e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSRLARAKVR 12

Db 3 KVHGSRLARAKVR 14

RESULT 10

ribosomal protein S30.e, cytosolic - yeast (*Saccharomyces cerevisiae*)

N:Alternate names: protein O4725; protein YLR287C-e; protein YOR182c

C:Species: *Saccharomyces cerevisiae*

C:Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 21-Jul-2000

C:Accession: S67074; S70775; S70776; S70774

R:Hughes, B.; Pohl, T.M.

submitted to the Protein Sequence Database, July 1996

A:Reference number: S66685

A:Accession: S67074

A:Molecule type: DNA

A:Residues: 1-63 <HUG>

A:Cross-references: EMBL:Z75090; GSPDB:GN00015; MIPS:YOR182c; NID:g1420438; PIDN:CAA

A:Experimental source: strain S288C

C:Genetics: YS30B

J: Baker, R.T.; Williams, N.A.; Wellenham, R.E.H.

J. Biol. Chem. 271, 13549-13555, 1996

A:Title: The yeast homolog of mammalian ribosomal protein S30 is expressed from a du

A:Reference number: S70774; MUID:96278780; PMID:8662789

A:Accession: S70775

A:Molecule type: DNA

A:Residues: 1-63 <BAK>

A:Cross-references: EMBL:U48700; NID:g1256752; PIDN:AAC49316.1; PID:g1256753

A:Genetics: YS30A

A:Accession: S70776

A:Molecule type: mRNA

A:Residues: 1-63 <BAV>

A:Cross-references: EMBL:U48699; NID:g1256750; PIDN:AAC49316.1; PID:g1256751

A:Genetics: YS30A

A:Accession: S70774

A:Molecule type: protein

A:Residues: 2-63 <BA3>

C:Genetics: <YS30B>

A:Gene: SCD:RPS30B; MIPS:YOR182c

A:Cross-references: MIPS:YOR182c; SGD:S0005708
 A:Map position: 15R
 A:introns: 1/3
 C:Genetics: <Y930A>
 A:Gene: SGD-RPS30A; MIPS:YLR287c-a
 A:Cross-references: MIPS:YLR287c-a; SGD:S0004278
 A:Map position: 12R
 A:introns: 1/3
 C:Superfamily: yeast ribosomal protein S30.e
 C:Keywords: cytosol; protein biosynthesis; ribosome
 F:2-63/Product: ribosomal protein S30.e, cytosolic #status experimental <MAT>

Query Match 20.3%; Score 12; DB 1; Length 63;
 Best Local Similarity 100.0%; Pred. No. 4,9e-05;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVHGLARAGV 12
 |||||
 Db 3 KVHGLARAGV 14

RESULT 11

A97094
 uncharacterized protein, YJDF B. subtilis ortholog [Imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: A97094
 R:Noilling, J.; Breton, G.; Omeichenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Bacteriol. 183; 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: A97094
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-135 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK79540.1; PID:G15024526; GSPDB:GN00168
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC1573

Query Match 13.6%; Score 8; DB 2; Length 135;
 Best Local Similarity 100.0%; Pred. No. 0.97;
 Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 21 KOEKKKKK 28
 |||||
 Db 124 KOEKKKKK 131

RESULT 12

S02776
 DNA-binding protein H-NS - Proteus vulgaris
 C:Species: Proteus vulgaris
 C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 13-Sep-1998
 C:Accession: S02776
 R:la Teana, A.; Falconi, M.; Scarlato, V.; Iammi, M.; Pon, C.L.
 FEBS Lett. 244; 34-38, 1989
 A:Title: Characterization of the structural genes for the DNA-binding protein H-NS in E.
 A:Reference number: S02775; MUID:89171270; PMID:2494066
 A:Accession: S02776
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-134 <LA1>
 C:Genetics:
 A:Gene: hns
 C:Function:
 A:Description: binds double-stranded DNA; influences regulation of gene expression at tr
 C:Superfamily: DNA-binding protein H-NS
 C:Keywords: DNA binding; transcription regulation

Query Match 11.9%; Score 7; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.8;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 28 KTRAKR 34
 |||||
 Db 83 KTRAKR 89

RESULT 13

B75305
 hypothetical protein - Deinococcus radiodurans (strain R1)
 C:Species: Deinococcus radiodurans
 C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 31-Mar-2000
 C:Accession: B75305
 R:White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.
 M.; Shen, M.; Vamathevan, J.J.; Lam, P.; McDonald, L.; Utterback, T.; Zalewski, C.
 S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
 Science 286; 1571-1577, 1999
 A:Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
 A:Reference number: A75250; MUID:20036896; PMID:10567266
 A:Accession: B75305
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-154 <WHI>
 A:Cross-references: GB:AE002051; GB:AE000513; NID:96459976; PIDN:AAF11732.1; PID:964
 A:Experimental source: strain R1
 C:Genetics:
 A:Gene: DR2179
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 154;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 RAKVRG 14
 |||||
 Db 39 RAKVRG 45

RESULT 14

E84782
 probable homeodomain transcription factor [Imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001
 C:Accession: E84782
 R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beutlo, M.I.; Town, C.D.; Fujii, C.Y.
 M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
 euse, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
 Nature 402; 761-768, 1999
 A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
 A:Reference number: A84420; MUID:20083487; PMID:10617197
 A:Accession: E84782
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-199 <STO>
 A:Cross-references: GB:AE002093; NID:94415906; PIDN:AAD20137.1; GSPDB:GN00139
 C:Genetics:
 A:Gene: AT2G36610
 A:Map position: 2

Query Match 11.9%; Score 7; DB 2; Length 199;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKK 28
 |||||
 Db 68 OEKKKK 74

RESULT 15

I52523
 nucleoporin p62 homolog - rat (fragment)
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 27-Feb-1997 #sequence_revision 27-Feb-1997 #text_change 05-Nov-1999

C:Accession: I52523
 R:Wang, Z.Q.; Akmal, K.M.; Kim, K.H.
 Biol. Reprod. 51, 1022-1030, 1994
 A:Title: An unusual nucleoprotein-related messenger ribonucleic acid is present in the ger
 A:Reference number: I52523; MUID:95151924; PMID:7849178
 A:Accession: I52523
 A:Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: mRNA
 A:Residues: 1-215 <RES>
 A:Cross-references: GB:S75997; NID:g913245; PIDN:AB33384.1; PID:g913246
 A:Experimental source: testis

Query Match 11.9%; Score 7; DB 2; Length 215;
 Best Local Similarity 100.0%; Pred. No. 14;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 EKKKKKTG 30
 |||||
 DB 52 KKKKKTG 58

RESULT 16
 H86318
 Probable 60S ribosomal protein L6 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: H86318
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: H86318
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <STO>
 A:Cross-references: GB:AE005172; NID:g9795602; PIDN:AF98420.1; GSPDB:GN00141
 C:Genetics:
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
 |||||
 DB 166 EKKKKKT 172

RESULT 17
 D96768
 Protein 60S ribosomal protein L6 P2P9.8 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: D96768
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso,
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.;
 Ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000
 A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.
 C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon,
 Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: D96768

A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <STO>
 A:Cross-references: GB:AE005173; NID:g7109467; PIDN:AF36731.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F2P9.8
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
 |||||
 DB 166 EKKKKKT 172

RESULT 18
 E96768
 Protein 60S ribosomal protein L6 P2P9.7 [imported] - Arabidopsis thaliana
 C:Species: Arabidopsis thaliana (mouse-ear cress)
 C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
 C:Accession: E96768
 R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alo
 Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar,
 Ansen, N.F.; Hughes, B.; Hulzar, L.
 Nature 408, 816-820, 2000

A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim
 C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziani,
 Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
 A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tall
 ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
 A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
 A:Reference number: A86141; MUID:21016719; PMID:11130712
 A:Accession: E96768
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-233 <STO>
 A:Cross-references: GB:AE005173; NID:g7109466; PIDN:AF36730.1; GSPDB:GN00141
 C:Genetics:
 A:Gene: F2P9.7
 A:Map position: 1

Query Match 11.9%; Score 7; DB 2; Length 233;
 Best Local Similarity 100.0%; Pred. No. 15;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
 |||||
 DB 166 EKKKKKT 172

RESULT 19
 T47174
 Hypothetical protein DKFZp7621166.1 - human (fragment)
 C:Species: Homo sapiens (man)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 02-Sep-2000
 C:Accession: T47174
 R:Blocker, H.; Boecher, M.; Brandt, P.; Mewes, H.W.; Well, B.; Wiemann, S.
 submitted to the Protein Sequence Database, March 2000
 A:Reference number: Z24376
 A:Accession: T47174
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-283 <AAA>
 A:Cross-references: EMBL:AL162072
 A:Experimental source: adult melanoma (Mewo cell line); clone DKFZp7621166
 C:Genetics:
 A:Note: DKFZp7621166.1
 C:Superfamily: unassigned WD repeat proteins; WD repeat homology
 Query Match 11.9%; Score 7; DB 2; Length 283;
 Best Local Similarity 100.0%; Pred. No. 18;

Matches 7: Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GSLARAG 10
|||||||
Db 236 GSLARAG 242

RESULT 20

D70313

riboflavin kinase - Aquifex aeolicus

C:Species: Aquifex aeolicus

C:Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 20-Sep-1999

C:Accession: D70313

R:Decker, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.; Ov

V.

Nature 392, 353-358, 1998

A:Title: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.

A:Reference number: A70300; MUID:98196666; PMID:9537320

A:Accession: D70313

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-314 <AQF>

A:Cross-references: GB:AE000675; NID:g2982863; PIDN:AC06488.1; PID:g2982868; GB:AE00065

A:Experimental source: strain VF5

C:Genetics:

A:Gene: rbf

C:Superfamily: conserved hypothetical protein H10963

Query Match

Best Local Similarity 11.9%; Score 7; DB 2; Length 314;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 47 PTFGKK 53
|||||||

Db 253 PTFGKK 259

RESULT 21

T19629

hypothetical protein C32A3.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999

C:Accession: T19629

R:Thomas, K.

submitted to the EMBL Data Library, February 1995

A:Reference number: Z19154

A:Accession: T19629

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-346 <WIL>

A:Cross-references: EMBL:Z48241; PIDN:CAA8285.1; GSPDB:GN00021; CESP:C32A3.2

A:Experimental source: clone C32A3

C:Genetics:

A:Gene: CESP:C32A3.2

A:Map position: 3

A:Introns: 47/3; 79/3; 111/2; 165/2; 266/1

Query Match

Best Local Similarity 11.9%; Score 7; DB 2; Length 346;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 23 EKKKKKT 29
|||||||

Db 6 EKKKKKT 12

RESULT 22

T36154

Probable ABC-type transport system ATP-binding protein - Streptomyces coelicolor

C:Species: Streptomyces coelicolor

C:Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 03-Dec-1999

C:Accession: T36154

R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.

submitted to the EMBL Data Library, July 1999

A:Reference number: Z21598

A:Accession: T36154

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-424 <SEB>

A:Cross-references: EMBL:AL096852; PIDN:CAB51012.1; GSPDB:GN00070; SCOEDB:SCE19A.31

A:Experimental source: strain A3(2)

C:Genetics:

A:Gene: SCOEDB:SCE19A.31

Query Match

Best Local Similarity 11.9%; Score 7; DB 2; Length 424;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GSLARAG 10
|||||||

Db 328 GSLARAG 334

RESULT 23

E84153

replicative DNA helicase dnaC [imported] - Bacillus halodurans (strain C-125)

C:Species: Bacillus halodurans

C:Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001

C:Accession: E84153

R:Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii, F.;

Nucleic Acids Res. 28, 4317-4331, 2000

A:Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans

A:Reference number: A83650; MUID:20512582; PMID:11058132

A:Accession: E84153

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-454 <STO>

A:Cross-references: GB:AP001520; GB:BA000004; NID:g10176401; PIDN:BA07748.1; GSPDB:

A:Experimental source: strain C-125

C:Genetics:

A:Gene: dnaC

C:Superfamily: phage P22 gene 12 protein

Query Match

Best Local Similarity 11.9%; Score 7; DB 2; Length 454;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 4 GSLARAG 10
|||||||

Db 281 GSLARAG 287

RESULT 24

T49516

Atu related protein [imported] - Neurospora crassa

N:Alternate names: protein B14D6.680

C:Species: Neurospora crassa

C:Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 02-Jun-2000

C:Accession: T49516

R:Schulte, U.; Algn, V.; Hohelsel, J.; Brandt, P.; Fartmann, B.; Holland, R.; Nyakati

submitted to the Protein Sequence Database, May 2000

A:Reference number: Z25022

A:Accession: T49516

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-710 <SCH>

A:Cross-references: EMBL:AL356173; GSPDB:GN00116; NCSP:B14D6.680

A:Experimental source: BAC clone B14D6; strain OR74A

C:Genetics:

A:Gene: NCSP:B14D6.680

A:Map position: 6

A:Introns: 422/1

Query Match

Best Local Similarity 11.9%; Score 7; DB 2; Length 710;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKK 28
|111111|
Db 700 OEKKKK 706

RESULT 25

F85343
hypothetical protein Atg29450 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cross)
C:Date: 16-Feb-2001 #sequence_revision 16-Feb-2001 #text_change 17-May-2002
C:Accession: F85343
R:Anonymous, The European Union Arabidopsis Genome Sequencing Consortium, The Cold Spring
Nature 402, 769-777, 1999
A:title: Sequence and analysis of chromosome 4 of the plant Arabidopsis thaliana.
A:Reference number: A85001; MUID:20083488; PMID:10617198
A:Map position: 4
A:Gene: Atg29450
C:Genetics:
A:cross-references: GB:NC_001268; NID:g7269844; PIDN:CAB79703.1; GSPDB:GN00140
A:Map position: 4
C:superfamily: unassigned Ser/Thr or Tyr-specific protein kinases; protein kinase homolo

Query Match 11.9%; Score 7; DB 2; Length 863;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKK 28
|111111|
Db 504 OEKKKK 510

RESULT 26

J01979
structural polypeptide - Venezuelan equine encephalitis virus (subtype I, strain Menatt)
N:contants: 6K protein; coat protein; membrane glycoprotein E1; membrane glycoprotein E2
C:Species: Venezuelan equine encephalitis virus
C:Date: 17-Feb-1994 #sequence_revision 17-Feb-1994 #text_change 16-Jul-1999
C:Accession: J01979
R:Neider, J.M.; Kinney, R.M.; Tsuchiya, K.R.; Trent, D.W.
J. Gen. Virol. 74, 519-523, 1993
A:title: Molecular evidence that epizootic Venezuelan equine encephalitis (VEE) I-AB vir
A:Reference number: J01978; MUID:93187617; PMID:8445371
A:Accession: J01979
A:Molecule type: mRNA
A:Residues: 1-1254 <SNE>
A:cross-references: GB:I04599; NID:g290619; PIDN:AAA2990.1; PID:g290621
C:superfamily: togavirus structural polypeptide
C:Keywords: coat protein; glycoprotein; polypeptide; transmembrane protein
F:1-274/Product: coat protein #status predicted <CTP>
F:275-333/Product: membrane glycoprotein E1 #status predicted <MG3>
F:334-756/Product: membrane glycoprotein E2 #status predicted <MG2>
F:701-721/Domain: transmembrane #status predicted <TM1>
F:757-812/Product: 6K protein #status predicted <KP6>
F:94-813/Domain: transmembrane #status predicted <TM2>
F:813-1254/Product: membrane glycoprotein E1 #status predicted <MG1>
F:1231-1248/Domain: transmembrane #status predicted <TM3>
F:47,285,651,946/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 11.9%; Score 7; DB 1; Length 1254;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKTC 30
|111111|
Db 88 KKKKTC 94

RESULT 27

B71619

hypothetical protein PFB0280w - malaria parasite (Plasmodium falciparum)

C:Species: Plasmodium falciparum
C:Date: 13-Nov-1998 #sequence_revision 13-Nov-1998 #text_change 21-Jul-2000
C:Accession: B71619
R:Gardner, M.J.; Tetteijn, H.; Carucci, D.J.; Cummings, L.M.; Aravind, L.; Koonin, E.
; Perera, M.; Salzberg, S.; Zhou, L.; Sutton, G.G.; Clayton, R.; White, O.; Smith, H
Science 282, 1126-1132, 1998
A:title: Chromosome 2 sequence of the human malaria parasite Plasmodium falciparum.
A:Reference number: A71600; MUID:99021743; PMID:9604551
A:Accession: B71619
A:Status: preliminary; nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-2539 <GAR>
A:cross-references: GB:AE001384; GB:AE001362; NID:g3845139; PIDN:MAC71845.1; PID:g384
A:Experimental source: clone 3D7
C:Genetics:
A:Gene: PFB0280w

Query Match 11.9%; Score 7; DB 2; Length 2539;
Best Local Similarity 100.0%; Pred. No. 11e+02;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKK 28
|111111|
Db 692 OEKKKK 698

RESULT 28

T28799
hypothetical protein C16E9.5 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 18-Feb-2000
C:Accession: T28799
R:Giesel, C.
submitted to the EMBL Data Library, November 1995
A:Description: The sequence of C. elegans cosmid C16E9.
A:Reference number: Z20525
A:Accession: T28799
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-46 <GEI>
A:cross-references: EMBL:U039677; PIDN:AAC47959.1; GSPDB:GN00028; CESP:C16E9.5
A:Experimental source: strain Bristol N2; clone C16E9
C:Genetics:
A:Gene: CESP:C16E9.5
A:Map position: x

Query Match 10.2%; Score 6; DB 2; Length 46;
Best Local Similarity 100.0%; Pred. No. 41;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKK 28
|111111|
Db 2 EKKKKK 7

RESULT 29

B69830
hypothetical protein ynfD - Bacillus subtilis
C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 15-Oct-1999
C:Accession: B69830
R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
C.; Bron, S.; Brouillette, S.; Brusch, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.;
A.; Enlilich, S.D.; Emerson, P.T.; Eutlian, K.D.; Erlington, J.; Febret, C.; Ferrari,
Nature 390, 249-256, 1997
A:Authors: Roulier, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fume, S.; Gallizzi, A.; Gall
lech, J.; Harwood, C.R.; Henault, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Huilo, T
Koelter, P.; Koningsstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardino
A.; Authors: Leuber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mau
Y, M.; Ogawa, K.; Ogilawa, A.; Oudega, B.; Park, S.H.; Paro, V.; Pohl, T.M.; Portate
Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadate, Y.; Sato, T.; Scanl
A; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Seikiguchi, J.; Sekowska, A.; Se

akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.
 A:Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.
 A:Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
 A:Reference number: A69580; MUID:98044033; PMID:9384377
 A:Accession: B69830
 A:Status: preliminary; nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-67 <KUN>
 A:Cross-references: GB:Z99109; GB:AL009126; NID:q2633260; PIDN:CAB12859.1; PID:el183021;
 A:Experimental source: strain 168
 C:Genetics:
 A:Gene: ynfD

Query Match
 Best Local Similarity 10.2%; Score 6; DB 2; Length 67;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 23 EKKKK 28
 Db 46 EKKKK 51

RESULT 30
 H97135
 uncharacterized phage related protein [Imported] - *Clostridium acetobutylicum*
 C:Species: *Clostridium acetobutylicum*
 C:Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 14-Sep-2001
 C:Accession: H97135
 R:Rolling, J.; Breton, G.; Omelchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium *Clostridium acetobutylicum*
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: H97135
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-70 <KUR>
 A:Cross-references: GB:AE001437; PIDN:AAK79875.1; PID:q15024892; GSPDB:GN00168
 A:Experimental source: *Clostridium acetobutylicum* ATCC824
 C:Genetics:
 A:Gene: CAC1912

Query Match
 Best Local Similarity 10.2%; Score 6; DB 2; Length 70;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 29 TGRKR 34
 Db 19 TGRKR 24

RESULT 31
 T47434
 hypothetical protein T22K7.120 - *Arabidopsis thaliana*
 C:Species: *Arabidopsis thaliana* (mouse-ear cress)
 C:Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 20-Apr-2000
 C:Accession: T47434
 R:Rieger, M.; Mueller-Auer, S.; Zipp, M.; Schaefer, M.; Mewes, H.W.; Rudd, S.; Lemcke, K.
 submitted to the Protein Sequence Database, April 2000
 A:Reference number: 224459
 A:Accession: T47434
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-74 <RIE>
 A:Cross-references: EMBL:AL138641
 A:Experimental source: cultivar Columbia; BAC clone T22K7
 C:Genetics:
 A:Map position: 3
 A:Introns: 31/3
 A>Note: T22K7.120

Query Match 10.2%; Score 6; DB 2; Length 74;

Best Local Similarity 100.0%; Pred. No. 60;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 24 KKKKK 29
 Db 69 KKKKK 74

RESULT 32
 B82267
 exodeoxyribonuclease, small chain VC0891 [Imported] - *Vibrio cholerae* (strain N16961)
 C:Species: *Vibrio cholerae*
 C:Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 02-Feb-2001
 C:Accession: B82267
 R:Heidelberg, J.F.; Eisen, J.A.; Nelson, W.C.; Clayton, R.A.; Gwin, M.L.; Dodson, R.
 chardson, D.; Ermolaeva, M.D.; Yamthuevan, J.; Bas, S.; Qin, H.; Dragol, I.; Sellers
 1, R.R.; Meklanos, J.J.; Venter, J.C.; Fraser, C.M.
 Nature 406, 477-483, 2000
 A:Title: DNA Sequence of both chromosomes of the cholera pathogen *Vibrio cholerae*.
 A:Reference number: A82035; MUID:20406833; PMID:10952301
 A:Accession: B82267
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-80 <HEI>
 A:Cross-references: GB:AE004173; GB:AE003852; NID:q9655341; PIDN:AAF94053.1; GSPDB:GN
 A:Experimental source: serogroup O1; strain N16961; biotype El Tor
 C:Genetics:
 A:Gene: VC0891
 A:Map position: 1
 C:Superfamily: exodeoxyribonuclease VII small chain

Query Match
 Best Local Similarity 10.2%; Score 6; DB 2; Length 80;
 Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 5 SLARAG 10
 Db 44 SLARAG 49

RESULT 33
 S66013
 ribosomal protein S18 (rpsr) - *Bacillus subtilis*
 N:Alternate names: ribosomal protein BS21
 C:Species: *Bacillus subtilis*
 C:Date: 28-Oct-1996 #sequence_revision 13-Mar-1997 #text_change 21-Jul-2000
 C:Accession: S66013; S11368; A69701
 R:Ogasawara, N.; Nakai, S.; Yoshikawa, H.
 DNA Res. 1, 1-14, 1994
 A:Title: Systematic sequencing of the 180 kilobase region of the *Bacillus subtilis* ch
 A:Reference number: S65967; MUID:96051385; PMID:7584024
 A:Accession: S66013
 A:Status: nucleic acid sequence not shown; translation not shown
 A:Molecule type: DNA
 A:Residues: 1-81 <OGA>
 A:Cross-references: EMBL:D26185; NID:q467326; PIDN:BAV05219.1; PID:q467373
 A:Experimental source: strain 168
 A>Note: the nucleotide sequence was submitted to the EMBL Data Library, December 1993
 M:Hiso, K.I.; Otake, E.; Osawa, S.
 Mol. Gen. Genet. 185, 239-244, 1982
 A:Title: Purification and characterization of 30S ribosomal proteins from *Bacillus su*
 A:Reference number: S09561; MUID:82219212; PMID:6806564
 A:Accession: S11368
 A:Molecule type: protein
 A:Residues: 4-26 <HIC>
 A:Experimental source: strain 168
 A>Note: 20-ASP was also found
 R:Kunst, F.; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Ber
 C.; Bron, S.; Brouillet, S.; Brusch, C.V.; Caldwell, B.; Capiano, V.; Carter, N.M.;
 A.; Ehrlich, S.D.; Emerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari,
 Nature 390, 249-256, 1997
 A:Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Funai, S.; Galizzi, A.; Gal
 tech, J.; Harwood, C.R.; Henauf, A.; Hilbert, H.; Holsappel, S.; Hosono, S.; Hullo, M

Koetter, P.; Konigstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinois, A.; Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Mauey, Y., M.; Ogawa, K.; Ogihara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle, R.; Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadale, Y.; Sato, T.; Scanlon, A.; Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Serot, A.; Authors: Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Milners, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; Authors: Yoshikawa, H.F.; Zumbstein, E.; Yoshikawa, H.; Danchin, A.; Danchin, A.

A>Title: The complete genome sequence of the Gram-positive bacterium *Bacillus subtilis*.
A:Reference number: A69580; MUID:98044033; PMID:9384377
A:Accession: A69701
A:Status: nucleic acid sequence not shown; translation not shown
A:Molecule type: DNA
A:Residues: 1-81 <RND>
A:Cross-references: GB:299124; GB:AL009126; NID:92636442; PIDN:CAB16126.1; PID:92636636
A:Experimental source: strain 168
C:Genetics:
A:Gene: rpsR
C:Superfamily: Escherichia coli ribosomal protein S18
C:Keywords: acetylated amino end; protein biosynthesis; ribosome
F:4-81/Product: ribosomal protein S18 #status experimental <MAT>
F:4/Modified site: acetylated amino end (Ala) (in mature form) #status experimental

Query Match 10.2%; Score 6; DB 2; Length 81;
Best Local Similarity 100.0%; Pred. No. 65;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 30 GRAKRR 35
|||||
Db 10 GRAKRR 15

RESULT 34
T36134
hypothetical protein SCE19A.11c - Streptomyces coelicolor
C:Species: Streptomyces coelicolor
C:Date: 03-Dec-1999 #sequence_rev150n 03-Dec-1999 #text_change 19-Jan-2001
C:Accession: T36134
R:Seeger, K.; Harris, D.; James, K.D.; Parkhill, J.; Barrell, B.G.; Rajandream, M.A.
Submitted to the EMBL Data Library, July 1999
A:Reference number: Z21598
A:Accession: T36134
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-92 <SEF>
A:Cross-references: EMBL:AL096852; PIDN:CAB50992.1; GSPDB:GN00070; SCOEDB:SCE19A.11c
A:Experimental source: strain A3(2)
C:Genetics:
A:Gene: SCOEDB:SCE19A.11c
C:Superfamily: probable sulfur carrier protein slr0821

Query Match 10.2%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 40 RRFVNV 45
|||||
Db 53 RRFVNV 58

RESULT 35
H82867
transcription regulator xfa0057 [imported] - *Xylella fastidiosa* (strain 9a5c)
C:Species: *Xylella fastidiosa*
C:Date: 18-Aug-2000 #sequence_rev150n 20-Aug-2000 #text_change 02-Sep-2000
C:Accession: H82867
R:anonymous, The *Xylella fastidiosa* Consortium of the Organization for Nucleotide Sequencing
Nature 406, 151-157, 2000
A>Title: The genome sequence of the plant pathogen *Xylella fastidiosa*.
A:Reference number: A82515; MUID:20355717; PMID:10910347
A:Note: for a complete list of authors see reference number A59328 below
A:Accession: H82867
A:Status: preliminary

A:Molecule type: DNA
A:Residues: 1-92 <STM>
A:Cross-references: GB:AE003851; NID:99112238; PIDN:AAF65625.1; GSPDB:GN00130; XFSC:
A:Experimental source: strain 9a5c
R:Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Birones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrei as-Neto, E.; Docena, C.; El-Dorri, H.; Facincani, A.P.; Ferreira, A.J.S.
Submitted to Genbank, June 2000
A:Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franco, S.C.; Franco, M.C.; Pi J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Le Chado, M.A.; Madeira, A.M.B.N.; Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins A:Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C., F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Savi A:Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, W.A.; de Sa, R.G.; Santelli, R.V.; Savi M.; Tshibabo, M.H.; Vallada, H.; Van Sluys, M.A.; Verjovsky-Almeida, S.; Vettore, A.L.
A:Reference number: A59328
A:Contents: annotation
C:Genetics:
A:Gene: xfa0057
A:Genome: plasmid
A:Note: plasmid pXF5.1

Query Match 10.2%; Score 6; DB 2; Length 92;
Best Local Similarity 100.0%; Pred. No. 72;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 31 RAKRRM 36
|||||
Db 12 RAKRRM 17

RESULT 36
H96585
hypothetical protein F20D21.23 [imported] - *Arabidopsis thaliana*
C:Species: *Arabidopsis thaliana* (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_rev150n 02-Mar-2001 #text_change 31-Mar-2001
C:Accession: H96585
R:Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alor Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Hultzer, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luero, J.S.; Maitl, R.; Maritz Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.; Shim, P.; Southwick, A.M.; Sun, H.; Talic ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A>Title: Sequence and analysis of chromosome 1 of the plant *Arabidopsis*.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: H96585
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-98 <STO>
A:Cross-references: GB:AE005173; NID:94585983; PIDN:AAD25619.1; GSPDB:GN00141
C:Genetics:
A:Gene: F20D21.23
A:Map position: 1

Query Match 10.2%; Score 6; DB 2; Length 98;
Best Local Similarity 100.0%; Pred. No. 76;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKK 28
|||||
Db 71 EKKKKK 76

RESULT 37
T07078
cold stress protein SRCL - soybean
C:Species: Glycine max (soybean)
C:Date: 30-Apr-1999 #sequence_rev150n 30-Apr-1999 #text_change 20-Jun-2000
C:Accession: T07078

R.Takahashi, R.; Shimosaka, E.

Plant. Sci. 123, 93-104, 1997

A>Title: CDNA sequence analysis and expression of two cold-regulated genes in soybean.

A:Reference number: Z15902

A:Accession: T07078

A:Status: preliminary; translated from GB/EMBL/DDBJ

A:Molecule type: mRNA

A:Residues: 1-102 <YAK>

A:Cross-references: EMBL:AB000129; PIDN:BAA19768.1

A:Experimental source: cultivar Kitamumume

C:Genetics:

A:Gene: srcl

C:Superfamily: cold stress protein COR19

C:Keywords: cold shock

Query Match

Best Local Similarity 10.2%; Score 6; DB 2; Length 102;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28

DB 76 EKKKKK 81

RESULT 38

CB7604

virulence-associated protein, probable [imported] - Caulobacter crescentus

C:Species: Caulobacter crescentus

C:Date: 20-Apr-2001 #sequence_revision 20-Apr-2001 #text_change 20-Apr-2001

C:Accession: CB7604

R:Neeman, W.C.; Feldblum, T.V.; Paulsen, I.T.; Nelson, K.E.; Eisen, J.; Heidelberg, J.

B.; Laub, M.T.; Deboy, R.T.; Dodson, R.J.; Durkin, A.S.; Gwin, M.L.; Haft, D.H.; Kolon

n, J.; Ermolaeva, M.; White, O.; Salzberg, S.L.; Shapiro, L.; Venter, J.C.; Fraser, C.M.

Proc. Natl. Acad. Sci. U.S.A. 98, 4136-4141, 2001

A>Title: Complete Genome Sequence of Caulobacter crescentus.

A:Reference number: A87249; MUID:21173698; PMID:1125647

A:Accession: CB7604

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-104 <STO>

A:Cross-references: GB:AE005673; NID:q13424481; PIDN:AAK24831.1; GSPDB:GN00148

C:Genetics:

A:Gene: CC2867

Query Match

Best Local Similarity 10.2%; Score 6; DB 2; Length 104;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 12 VRGQTP 17

DB 51 VRGQTP 56

RESULT 39

PM0017

hypothetical protein 105 (gsm 3' region) - Micromonospora purpurea (fragment)

C:Species: Micromonospora purpurea

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994

C:Accession: PM0017

R:Kleimen, G.H.; Cundliffe, E.; Financsek, I.

Gene 98, 53-60, 1991

A>Title: Cloning and characterization of gentamicin-resistance genes from Micromonospora

A:Reference number: JG0017; MUID:91192615; PMID:2013410

A:Accession: PM0017

A:Molecule type: DNA

A:Residues: 1-105 <KEU>

A:Cross-references: GB:M55520

A>Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe and

C:Keywords: antibiotic resistance

Query Match

Best Local Similarity 10.2%; Score 6; DB 2; Length 105;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10

DB 11 SLARAG 16

RESULT 40

PM0018

hypothetical protein 105 - Micromonospora sp. (fragment)

C:Species: Micromonospora sp.

C:Date: 30-Sep-1991 #sequence_revision 30-Sep-1991 #text_change 28-Oct-1994

C:Accession: PM0018

R:Kleimen, G.H.; Cundliffe, E.; Financsek, I.

Gene 98, 53-60, 1991

A>Title: Cloning and characterization of gentamicin-resistance genes from Micromonospora

A:Reference number: JG0017; MUID:91192615; PMID:2013410

A:Accession: PM0018

A:Molecule type: DNA

A:Residues: 1-105 <KEU>

A:Cross-references: GB:M55521

A>Note: the authors translated the codon CCG for residues 27, 30, 31, and 37 as Phe and

Query Match

Best Local Similarity 10.2%; Score 6; DB 2; Length 105;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAG 10

DB 11 SLARAG 16

RESULT 41

S59536

cold stress protein COR1 - Poncirus trifoliata

C:Species: Poncirus trifoliata

C:Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 24-Sep-1999

C:Accession: S59536

R:Cal, Q.; Moore, G.A.; Guy, C.L.

Plant Mol. Biol. 29, 11-23, 1995

A>Title: An unusual group 2 LEA gene family in citrus responsive to low temperature.

A:Reference number: S59534; MUID:96017610; PMID:7579157

A:Accession: S59536

A:Status: translation not shown

A:Molecule type: mRNA

A:Residues: 1-106 <CAI>

A:Cross-references: EMBL:L39005; NID:9625154; PIDN:AAA99963.1; PID:9625155

A:Experimental source: seedling; tissue type leaf

C:Superfamily: cold stress protein COR19

C:Keywords: cold shock

Query Match

Best Local Similarity 10.2%; Score 6; DB 2; Length 106;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKK 28

DB 87 EKKKKK 92

RESULT 42

S69849

hypothetical protein YMR290w-a - yeast (Saccharomyces cerevisiae)

C:Species: Saccharomyces cerevisiae

C:Date: 23-Aug-1996 #sequence_revision 06-Sep-1996 #text_change 26-Aug-1999

C:Accession: S69849

R:Barrell, B.G.

submitted to the EMBL Data Library, August 1994

A:Reference number: S47445

A:Accession: S69849

A:Molecule type: DNA

A:Residues: 1-115 <BAR>

A:Cross-references: EMBL:X80836; MIPS:YMR290w-a

C:Genetics:

A:Map position: 13R
C:Superfamily: Saccharomyces hypothetical protein YMR290W-a

Query Match 10.2%; Score 6; DB 2; Length 115;
Best Local Similarity 100.0%; Pred. No. 87;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
DB 98 EKKKK 103

RESULT 43

H84651

hypothetical protein Atg25720 (imported) - Arabidopsis thaliana

C:Species: Arabidopsis thaliana (mouse-ear cress)

C>Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 02-Feb-2001

C:Accession: H84651

R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Beilto, M.I.; Town, C.D.; Fujii, C.Y.;

M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

Nuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

Nature 402, 761-768, 1999

A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.

A:Reference number: A84420; MUID:20083487; PMID:10617197

A:Accession: H84651

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-117 <STO>

A:Cross-references: GB:AE002093; NID:g4874310; PIDN:AAD31372.1; GSPDB:GN00139

C:Genetics:

A:Gene: Atg25720

A:Map position: 2

Query Match 10.2%; Score 6; DB 2; Length 117;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
DB 27 EKKKK 32

RESULT 44

B71268

probable ribosomal protein L19 (rplS) - syphilis spirochete

C:Species: Treponema pallidum subsp. pallidum (syphilis spirochete)

C>Date: 24-Jul-1998 #sequence_revision 24-Jul-1998 #text_change 13-Aug-1999

C:Accession: B71268

R:Fraser, C.M.; Norris, S.J.; Weinstein, G.M.; White, O.; Sutton, G.G.; Dodson, R.; Gwin

rson, J.; Khalak, H.; Richardson, D.; Howell, J.K.; Childamarram, M.; Uterback, T.; MCD

they, L.; Weidman, J.; Smith, H.O.; Venter, J.C.

Science 281, 375-388, 1998

A:Title: Complete genome sequence of Treponema pallidum, the syphilis spirochete.

A:Reference number: A71250; MUID:98332770; PMID:9665876

A:Accession: B71268

A:Status: preliminary; nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-123 <COL>

A:Cross-references: GB:AE001259; GB:AE000520; NID:g3323209; PIDN:AAC65861.1; PID:g332322

A:Experimental source: strain Nichols

C:Genetics:

A:Gene: TP0909

C:Superfamily: Escherichia coli ribosomal protein L19

Query Match 10.2%; Score 6; DB 2; Length 123;
Best Local Similarity 100.0%; Pred. No. 92;

Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 8 RAGKV 13
|||||
DB 89 RAGKV 94

RESULT 45

R3R725

ribosomal protein S25, cytosolic (validated) - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jul-2000

C:Accession: A38969; S17353

R:Chan, Y.L.; Wool, I.G.

Biochem. Biophys. Res. Commun. 186, 1688-1693, 1992

A:Title: The primary structure of rat ribosomal protein S25.

A:Reference number: JH0691; MUID:92378645; PMID:1354961

A:Accession: A38969

A:Molecule type: mRNA

A:Residues: 1-125 <CH2>

A:Cross-references: EMBL:X62482; NID:g57723; PIDN:CAA44349.1; PID:g57724

A>Note: the protein is designated as ribosomal protein S25 by comparison to the comp

C:Superfamily: rat ribosomal protein S25

C:Keywords: protein biosynthesis; ribosome

Query Match 10.2%; Score 6; DB 1; Length 125;
Best Local Similarity 100.0%; Pred. No. 93;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSLAR 9
|||||
DB 81 GSLAR 86

Search completed: February 6, 2003, 21:32:13
Job time : 21 secs

GenCore version 5.1.3
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 21:29:24 : Search time 29 Seconds
(Without alignments)
419.199 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KVHSLARAGKVRGQTPKVA.....RFEVNVVPTFGKKKGPANNS 59

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 671580 seqs, 206047115 residues

Word size : 0

Total number of hits satisfying chosen parameters: 671580

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

SPREMBL_21:*

- 1: sp_archaea:*
- 2: sp_bacteria:*
- 3: sp_fungi:*
- 4: sp_human:*
- 5: sp_invertebrate:*
- 6: sp_mammal:*
- 7: sp_mhc:*
- 8: sp_organelle:*
- 9: sp_phage:*
- 10: sp_plant:*
- 11: sp_rodent:*
- 12: sp_virus:*
- 13: sp_vertebrate:*
- 14: sp_unclassified:*
- 15: sp_virus:*
- 16: sp_bacteriaph:*
- 17: sp_archaeap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	59	100.0	133	4 Q9H5V4	Q9H5V4 homo sapien
2	59	100.0	133	11 Q9J724	Q9J724 mus musculu
3	59	100.0	137	11 Q920W8	Q920W8 mus musculu
4	59	100.0	137	11 Q920W7	Q920W7 mus splicile
5	59	100.0	137	11 Q91V99	Q91V99 mus musculu
6	23	39.0	133	13 Q90YPI	Q90YPI Ictaelurus p
7	22	37.3	62	10 Q9M0E4	Q9M0E4 arabidopsis
8	21	35.6	230	4 Q15351	Q15351 homo sapien
9	15	25.4	132	5 Q9VDH8	Q9VDH8 drosophila
10	13	22.0	130	5 Q18231	Q18231 caenorhabdi
11	12	20.3	131	5 Q962G1	Q962G1 spodoptera
12	9	15.3	309	10 Q9S3U0	Q9S3U0 arabidopsis
13	8	13.6	135	16 Q971R7	Q971R7 clostridium
14	7	11.9	134	2 Q9L657	Q9L657 proteus mir
15	7	11.9	154	16 Q9RSE5	Q9RSE5 delnoccocu
16	7	11.9	157	5 Q9NBB4	Q9NBB4 drosophila

17	7	11.9	173	10 Q9Z0B1	Q9Z0B1 arabidopsis
18	7	11.9	198	2 Q9ACU8	Q9ACU8 bruceella ab
19	7	11.9	215	11 Q64075	Q64075 rattus sp.
20	7	11.9	224	10 Q9L1R5	Q9L1R5 arabidopsis
21	7	11.9	233	10 Q9FZ76	Q9FZ76 arabidopsis
22	7	11.9	233	10 Q9C9C6	Q9C9C6 arabidopsis
23	7	11.9	233	10 Q9C9C5	Q9C9C5 arabidopsis
24	7	11.9	259	16 Q9AD23	Q9AD23 streptomyc
25	7	11.9	283	4 Q9NSK3	Q9NSK3 homo sapien
26	7	11.9	309	5 Q9ST41	Q9ST41 drosophila
27	7	11.9	314	16 Q65335	Q65335 aquilex aeo
28	7	11.9	339	5 Q95XC7	Q95XC7 caenorhabdi
29	7	11.9	380	4 Q96GN4	Q96GN4 homo sapien
30	7	11.9	380	5 Q9M0W6	Q9M0W6 drosophila
31	7	11.9	381	4 Q15694	Q15694 homo sapien
32	7	11.9	424	16 Q9S2F0	Q9S2F0 streptomyc
33	7	11.9	429	2 Q9X4J1	Q9X4J1 streptomyc
34	7	11.9	454	16 Q9K5Q9	Q9K5Q9 bacillus ha
35	7	11.9	542	13 Q91290	Q91290 pleurodeles
36	7	11.9	575	4 Q9NXU4	Q9NXU4 homo sapien
37	7	11.9	594	16 Q98CL9	Q98CL9 thizobium l
38	7	11.9	806	10 Q9M6T5	Q9M6T5 arabidopsis
39	7	11.9	863	10 Q9M0D8	Q9M0D8 arabidopsis
40	7	11.9	1254	12 Q9WC26	Q9WC26 venezuelan
41	7	11.9	1254	12 Q9YKD3	Q9YKD3 venezuelan
42	7	11.9	1254	12 Q88979	Q88979 venezuelan
43	7	11.9	1254	12 Q8V293	Q8V293 venezuelan
44	7	11.9	1254	12 Q8V291	Q8V291 venezuelan
45	7	11.9	1264	12 Q8UYH1	Q8UYH1 venezuelan

ALIGNMENTS

RESULT 1

Q9H5V4 PRELIMINARY: PRT: 133 AA.

AC Q9H5V4: 01-MAR-2001 (TREMBLERel. 16, Created)
DT 01-MAR-2001 (TREMBLERel. 16, Last sequence update)
DT 01-DEC-2001 (TREMBLERel. 19, Last annotation update)
DE CDNA: FLJ22986 fis, clone KAT11742.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RA Watanabe K., Kunagai A., Itakura S., Yamazaki M., Tashiro H., Ota T.,
RA Suzuki Y., Ohayashi M., Nishi T., Shibahara T., Tanaka T.,
RA Nakamura Y., Iwagaki T., Sugano S.,
RT "NEDO human cDNA sequencing project."
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AK026639; BAB15515.1; -.
DR HSSP: P02248; IUBI.
DR InterPro: IPR000626; Ublgultln.
DR Pfam: PF00240; ublgultln; 1.
DR PRINTS: PR00348; UBLGULTIN.
DR SMART: SM00213; UBO; 1.
DR PROSITE: PS00299; UBIQUITIN_1; 1.
DR PROSITE: PS50053; UBIQUITIN_2; 1.
SQ SEQUENCE 133 AA; 14390 MW; 5D2F81F2A355B559 CMC64;

Query Match 100.0%; Score 59; DB 4; Length 133;
Best local Similarity 100.0%; Pred. No. 3.5e-86;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARAGKVRGQTPKVAQEKKKKTGAKRMQYNRRFVNVVPTFGKKKGPANNS 59
Db 75 KVHSLARAGKVRGQTPKVAQEKKKKTGAKRMQYNRRFVNVVPTFGKKKGPANNS 133

RESULT 2

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09J324
ID 09J324 PRELIMINARY: PRT: 133 AA.
AC 09J324:
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-DEC-2001 (Tremblrel. 19, Last annotation update)
DE Monoclonal non-specific suppressor factor beta (Finkel-Biskis-Reilly
DE murine sarcoma virus (FBR-MuSV) ubiquitously expressed) (fox
DE derived).
GN FAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=SWISS OB;
RA Nie G.-Y., Li Y., Salmons L.A., Clements J.A., Findlay J.K.;
RT "Identification of monoclonal non-specific suppressor factor beta as
RT one of the genes differentially expressed at implantation sites
RT compared to interimplantation sites in the mouse uterus.";
RL submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=SMALL INTESTINE AND KIDNEY;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Aikawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
RA Aikawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamataka I.,
RA Salto T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Salto R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fleischnann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schirml L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barish G.,
RA Blake J., Boffelli D., Bojunga N., Carrinci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seva T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
RA Wyshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
DR EMBL: AF147745; AAF80246.1; -;
DR EMBL: AK008466; BAB25684.1; -;
DR EMBL: AK002355; BAB22034.1; -;
DR HSSP: P02248; IUBT.
DR MGD: MGI:102347; Fau.
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin.1.
DR PRINTS: PR00348; UBIOUITIN.
DR SMART: SM00213; UBO.1.
DR PROSITE: PS00299; UBIOUITIN_1; 1.
DR PROSITE: PS50053; UBIOUITIN_2; 1.
SQ SEQUENCE 133 AA; 14416 MW; 2087C774A022AB16 CRC64;

Query Match 100.0%; Score 59; DB 11; Length 133;
Best Local Similarity 100.0%; Pred. No. 3.5e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPNN 59
Db 75 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPNN 133

RESULT 3
O920W8 PRELIMINARY: PRT: 137 AA.
AC 0920W8:
DT 01-DEC-2001 (Tremblrel. 19, Created)

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DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Fau protein (Fragment).
GN FAU.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BLG2/MSF;
RA Liu Y., Kitano T., Koide T., Shirosaki T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039086; BAB68610.1; -;
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin.1.
DR PROSITE: PS00299; UBIOUITIN_1; UNKNOWN_1.
DR PROSITE: PS50053; UBIOUITIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 137 AA; 14845 MW; 57099FF405D8B2B CRC64;

Query Match 100.0%; Score 59; DB 11; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.6e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPNN 59
Db 79 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPNN 137

RESULT 4
O920W7 PRELIMINARY: PRT: 137 AA.
AC 0920W7:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
DE Fau protein (Fragment).
GN FAU.
OS Mus spicilegus (Steppe mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10103;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=ZBN;
RA Liu Y., Kitano T., Koide T., Shirosaki T., Moriaki K., Saitou N.;
RT "Conspicuous Differences among Gene Genealogies of 21 Nuclear Genes of
RT Five Mus musculus subspecies.";
RL submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AB039093; BAB68617.1; -;
DR InterPro: IPR000626; Ubiquitin.
DR Pfam: PF00240; ubiquitin.1.
DR PROSITE: PS00299; UBIOUITIN_1; UNKNOWN_1.
DR PROSITE: PS50053; UBIOUITIN_2; 1.
FT NON_TER 1
SQ SEQUENCE 137 AA; 14787 MW; 57099FF7065D8828 CRC64;

Query Match 100.0%; Score 59; DB 11; Length 137;
Best Local Similarity 100.0%; Pred. No. 3.6e-56;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPNN 59
Db 79 KVGSLARAGKVGRTPPVAKOEKKKKTGRARRMOYNNRFVNVPTFGKKKGPNN 137

RESULT 5
O91V99 PRELIMINARY: PRT: 137 AA.
AC 091V99:
DT 01-DEC-2001 (Tremblrel. 19, Created)

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DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Fau protein (Fragment).
 GN FAU.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-VARIABLE STRAINS:
 RA Liu Y., Kitano T., Koide T., Shiroishi T., Moriwaki K., Saitou N.;
 RT "Conspicuous differences among Gene Genealogies of 21 Nuclear Genes of
 RT Five Mus musculus subspecies.";
 RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AB039084; BAB68608.1; -;
 DR EMBL; AB039085; BAB68609.1; -;
 DR EMBL; AB039087; BAB68611.1; -;
 DR EMBL; AB039088; BAB68612.1; -;
 DR EMBL; AB039089; BAB68613.1; -;
 DR EMBL; AB039090; BAB68614.1; -;
 DR EMBL; AB039091; BAB68615.1; -;
 DR EMBL; AB039092; BAB68616.1; -;
 DR InterPro: IPR000626; Ubligutlin.
 DR Pfam: PF00240; Ubligutlin.1.
 DR PROSITE: PS00299; UBIQUITIN_1; UNKNOWN_1.
 DR PROSITE: PS50053; UBIQUITIN_2; 1.
 FT NON_TER 1
 FT SEQUENCE 137 AA; 14787 MW; 57099FF7065D8828 CRC64;

Query Match 100.0%; Score 59; DB 11; Length 137;
 Best Local Similarity 100.0%; Pred. No. 3.6e-56;
 Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KHGSLARACKVRCQTPKVAKEKKKKKTGKAKRRMQYNRFVNVVPTFGKKKGNPANS 59
 Db 79 KHGSLARACKVRCQTPKVAKEKKKKKTGKAKRRMQYNRFVNVVPTFGKKKGNPANS 137

RESULT 6
 ID 090YPL PRELIMINARY; PRT; 133 AA.
 AC 090YPL:
 DT 01-DEC-2001 (TReMBLrel. 19, Created)
 DT 01-DEC-2001 (TReMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE 40S ribosomal protein S30.
 OS Ictalurus punctatus (Channel catfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Siluriformes;
 OC Ictaluridae; Ictalurus.
 OX NCBI_TaxID=7998;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Karsl A., Patterson A., Feng J., Liu Z.J.;
 RT "Translational machinery of channel catfish: I. A transcriptomic
 RT approach to the analysis of 32 40S ribosomal protein genes and their
 RT expression.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF402841; AAK95215.1; -;
 DR InterPro: IPR000626; Ubligutlin.
 DR Pfam: PF00240; Ubligutlin.1.
 DR PROSITE: PS50053; UBIQUITIN_2; 1.
 DR Ribosomal protein.
 KW Ribosomal protein.
 SO SEQUENCE 133 AA; 14504 MW; 62036BB0E72C5CNC CRC64;

Query Match 39.0%; Score 23; DB 13; Length 133;
 Best Local Similarity 100.0%; Pred. No. 4.1e-17;
 Matches 23; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 37 QYNRRFVNVVPTFGKKKGNPANS 59
 ||||||||||||||||||||||||

Db 111 QYNRRFVNVVPTFGKKKGNPANS 133

RESULT 7
 ID 09MOE4 PRELIMINARY; PRT; 62 AA.
 AC 09MOE4:
 DT 01-OCT-2000 (TReMBLrel. 15, Created)
 DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
 DE Ribosomal protein S30 homolog (40S ribosomal protein S30 homolog)
 DE (At2g19750/F6F22.22).
 GN AT2G29390.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsis.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-COLUMBIA;
 RX MEDLINE-98403884; PubMed-9734815;
 RA Kotani H., Nakamura Y., Sato S., Asamizu E., Kaneko T., Miyaajima N.,
 RA Tabata S.;
 RT "Structural analysis of Arabidopsis thaliana chromosome 5. VI.
 RT Sequence features of the regions of 1,367,185 bp covered by 19
 RT physically assigned P1 and TAC clones.";
 RL DNA Res. 5:203-216(1998).
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Shin P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C.,
 RA Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A.,
 RA Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X.,
 RA Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J.,
 RA Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A.,
 RA Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu S.,
 RA Shinozaki K., Davis R.W., Theologis A., Ecker J.R.;
 RT "Arabidopsis cDNA clones.";
 RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RA Kim C.J., Chen H., Cheuk R., Koesema E., Meyers M.C., Banh J.,
 RA Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
 RA Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
 RA Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
 RA Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou M.,
 RA Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
 RA Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
 RA Ecker J.R.;
 RT "Arabidopsis ORF clones.";
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AL161574; CAB79697.1; -;
 DR EMBL; AB013392; BAB09885.1; -;
 DR EMBL; AY052341; AAK96533.1; -;
 DR EMBL; AY061910; AAL31237.1; -;
 DR Ribosomal protein.
 KW Ribosomal protein.
 SO SEQUENCE 62 AA; 6887 MW; 95D8F3B72F53F33 CRC64;

Query Match 37.38%; Score 22; DB 10; Length 62;
 Best Local Similarity 100.0%; Pred. No. 2.4e-16;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 OY 1 KHGSLARACKVRCQTPKVAKO 22

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Db      3 KVGSLARAGKVGCGTPTKAVKO 24
|||||
RESULT 8
ID      015351      PRELIMINARY;      PRT;      230 AA.
AC      015351;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DE      01-JUN-2002 (TREMblrel. 21, Last annotation update)
DE      SEB4B (Fragment).
GN      SEB4B(HUMAN).
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;

RP      SEQUENCE FROM N.A.
RC      TISSUE=THYMUS;
RA      Ruehlmann A., Gupta A., Terhorst C.;
RT      "A novel murine RRM-type protein and its human homolog.";
RL      Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
DR      EMBL; X75315; CA53064.1; -.
DR      HSP; P09651; IUP1.
DR      InterPro: IPR000504; RNA_rec_mot.
DR      Pfam; PF00076; rrm; 1.
DR      SMART; SM00360; RRM; 1.
DR      PROSITE; PS50102; RRM; 1.
DR      PROSITE; PS00030; RRM_RNP_1;
FT      NON_TER
SQ      SEQUENCE      230 AA;      25220 MW;      C747D6500608461 CRC64;

Query Match      35.6%;      Score 21;      DB 4;      Length 230;
Best Local Similarity 100.0%;      Pred. No. 1e-14;
Matches      21;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

QY      34 RRMQYRRFVNVVPTFGKKKG 54
      |||||||
Db      1 RRMQYRRFVNVVPTFGKKKG 21

RESULT 9
QYVDH8      PRELIMINARY;      PRT;      132 AA.
AC      QYVDH8;
DT      01-MAY-2000 (TREMblrel. 13, Created)
DT      01-MAY-2000 (TREMblrel. 13, Last sequence update)
DT      01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE      CG15697 protein (RH08962p).
GN      CG15697.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC      Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BERKELEY;
RX      MEDLINE=20196006; PubMed-10731132;
RA      Adams M.D., Ceinliker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA      Amaratilake P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA      George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA      Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA      Brandon R.C., Rogers J.H.C., Blazej R.G., Champe M., Pfeiffer B.D.,
RA      Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA      Abri J.F., Agbayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA      Ballew R.M., Basu A., Baxendale J., Bayraktiroglu L., Beasley E.M.,
RA      Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
RA      Borovica D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
RA      Burdits K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA      Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA      de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,

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RA      Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA      Durbin K.J., Evangelista C.C., Feriaz C., Ferreira S., Fleischmann W.,
RA      Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA      Glodok A., Gong F., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA      Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA      Hostin D., Houston K.A., Howland T.J., Mei M.-H., Ibegwam C.,
RA      Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kelchum K.A.,
RA      Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA      Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
RA      Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA      Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
RA      Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
RA      Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Pacled J.M.,
RA      Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
RA      Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA      Shue B.C., Siden-Klamos I., Simpson M., Skupski M.P., Smith T.,
RA      Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA      Svrtkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA      Wang Z.-Y., Wasserman D.A., Weinstein G.M., Weissenbach J.,
RA      Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
RA      Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
RA      Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
RA      Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
RT      "The genome sequence of Drosophila melanogaster.";
RL      Science 287:2185-2195(2000).

RP      SEQUENCE FROM N.A.
RC      STRAIN=BERKELEY;
RA      Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
RA      Champe M., Chavez C., Dorsett V., Dresnek D., Farfan D., Fise E.,
RA      George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
RA      Miranda A., Mungall C.J., Nunoo J., Pacled J., Paragas V., Park S.,
RA      Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
RA      Ceinliker S.;
RL      Submitted (DEC-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL; AE003732; AAF55815.1; -.
DR      EMBL; AY071683; AAL49305.1; -.
DR      FlyBase; FBgn0038834; CG15697.
DR      InterPro: IPR000626; Ubiqultin.
DR      Pfam; PF00240; ubi1qultin; 1.
SQ      SEQUENCE      132 AA;      14585 MW;      E07C54F316FD5 CRC64;

Query Match      25.4%;      Score 15;      DB 5;      Length 132;
Best Local Similarity 100.0%;      Pred. No. 2e-08;
Matches      15;      Conservative      0;      Mismatches      0;      Indels      0;      Gaps      0;

QY      21 KOEKKKKKTGRARR 35
      |||||||
Db      93 KOEKKKKKTGRARR 107

RESULT 10
Q18231      PRELIMINARY;      PRT;      130 AA.
AC      Q18231;
DT      01-NOV-1996 (TREMblrel. 01, Created)
DT      01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT      01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE      C26f1.4 protein.
GN      C26f1.4.
OS      Caenorhabditis elegans.
OC      Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
OC      Rhabditidae; Peloderinae; Caenorhabditis.
OX      NCBI_TaxID=6239;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=BRISTOL N2;
RX      MEDLINE=94150718; PubMed-7906398;
RA      Wilson R., Almscough R., Anderson K., Baynes C., Berks M.,
RA      Bonfield J., Burton J., Connell M., Copey T., Cooper J., Coulson A.,
RA      Craxton M., Dear S., Du Z., Durbin R., Faveillo A., Fulton L.,
RA      Garner A., Green P., Hawkins T., Hillier L., Jier M., Johnston L.,
RA      Jones M., Kershaw J., Kirsten J., Laister N., Latreille P.,

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RA Lightning J., Lloyd C., McMurray A., Mortimore B., O'Callaghan M.,
RA Parsons J., Percy C., Rifken L., Roopra A., Saunders D., Showkeen R.,
RA Smailson N., Smith A., Sonhammer E., Staden R., Sulston J.,
RA Tillery-Mieg J., Thomas K., Vaudin M., Vaughan K., Waterson R.,
RA Watson A., Weinstock L., Wilkinson-Sproat J., Woldman P.,
RT "2.2 Mb of contiguous nucleotide sequence from chromosome III of C.
RT elegans";
RL Nature 368:32-38(1994).
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Geisel C., Stellyes L., Bradshaw H.;
RT "The sequence of C. elegans cmd C26F1.";
RL Submitted (APR-1996) to the EMBL/GenBank/DBJ databases.
RN [13]
RP SEQUENCE FROM N.A.
RC STRAIN-BRISTOL N2;
RA Waterson R.;
RL Submitted (NOV-1996) to the EMBL/GenBank/DBJ databases.
DR EMBL: U51148; AAB37076.1; -.
DR HSSP; P02248; IUBI.
DR InterPro: IPR000626; Ubiqutin.
DR Pfam: PF00240; ubiqutin; 1.
DR SMART: SM00213; UBO; 1.
SQ SEQUENCE 130 AA; 14033 MW; 50DC09AFB9F48532 CRC64;

Query Match 22.0%; Score 13; DB 5; Length 130;
Best Local Similarity 100.0%; Pred. No. 2.9e-06;
Matches 13; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARACKV 13
DB 72 KVHSLARACKV 84

RESULT 11
096201 PRELIMINARY; PRT; 131 AA.
AC 096201;
DT 01-DEC-2001 (TREMBLrel. 19, Created)
DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Ribosomal protein S30.
OS Spodoptera frugiperda (Fall armyworm).
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
OC Pterygota; Neoptera; Endopterygota; Lepidoptera; Glossata; Ditrysia;
OC Noctuidae; Noctuidae; Amphipyritae; Spodoptera.
OX NCBI_TaxID=7108;
RN [1]
RP SEQUENCE FROM N.A.
RA Landais I., Ogilastro M., Mita K., Nohata J., Lopez-Ferber M.,
RA Donot-Cerutti M., Fournier P., Devauchelle G.;
RT "Full-length ribosomal protein sequence from an EST library of
RT Spodoptera frugiperda cells (Sf9).";
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF400225; AAK92197.1; -.
SQ SEQUENCE 131 AA; 14314 MW; 03AE0E31EB1B04 CRC64;

Query Match 20.3%; Score 12; DB 5; Length 131;
Best Local Similarity 100.0%; Pred. No. 3.5e-05;
Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARACKV 12
DB 73 KVHSLARACKV 84

RESULT 12
09S9J0 PRELIMINARY; PRT; 309 AA.
AC 09S9J0;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)

DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE T23K8.1 (Fragment).
CN T23K8.1.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RA Vysotskaya V.S., Schwartz J.R., Yu G., Toriumi M., Lenz C., Liu S.,
RA Li J., Kremenetskaia I., Ngan I., Luros J., Gonzalez A., Altafi H.,
RA Araujo R., Chao Q., Conn L., Conway A.B., Dunn P., Hansen N.,
RA Huizar L., Kim C., Palm C.J., Rowley D., Shinn P., Walker M.,
RA Davis R.W., Ecker J.R., Federspiel N.A., Theologis A.;
RT "Arabidopsis thaliana chromosome 1 BAC T23K8 sequence.";
RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
RN [12]
RP SEQUENCE FROM N.A.
RC STRAIN-CV, COLUMBIA;
RA Theologis A.;
RL Submitted (MAY-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC007230; AAD26867.1; -.
FT NON TER 309
SQ SEQUENCE 309 AA; 34049 MW; 4FF1D7AF877A0D1 CRC64;

Query Match 15.3%; Score 9; DB 10; Length 309;
Best Local Similarity 100.0%; Pred. No. 0.14;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTGRA 32
DB 232 KKKKKTGRA 240

RESULT 13
0971R7 PRELIMINARY; PRT; 135 AA.
AC 0971R7;
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-OCT-2001 (TREMBLrel. 18, Last annotation update)
DE Uncharacterized protein, yJDF B. subtilis ortholog.
CN CAC1573.
OS Clostridium acetobutylicum.
OC Bacteria; Firmicutes; Bacillus/Clostridium group; Clostridia;
OC Clostridiales; Clostridaceae; Clostridium.
OX NCBI_TaxID=1488;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-ATCC 824 / DSM 792 / VKM B-1787;
RX MEDLINE=21359325; PubMed=11466286;
RA Noelling J., Breton G., Omelchenko M.V., Makarova K.S., Zeng Q.,
RA Gibson R., Lee H.M., Dubois J., Olu D., Hitti J., Wolf Y.I.,
RA Tatusov R.L., Sabathe P., Doucet-Stamm L., Soucaille P., Daly M.J.,
RA Bennett G.N., Koonin E.V., Smith D.R.;
RT "Genome sequence and comparative analysis of the solvent-producing
RT bacterium Clostridium acetobutylicum.";
RL J. Bacteriol. 183:4823-4838(2001).
DR EMBL: AE007667; AAK79540.1; -.
KW Complete proteome.
SQ SEQUENCE 135 AA; 16388 MW; 387D5F8D11444E7A CRC64;

Query Match 13.6%; Score 8; DB 16; Length 135;
Best Local Similarity 100.0%; Pred. No. 0.79;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KOEKKKK 28
DB 124 KOEKKKK 131

RESULT 14

09L657 PRELIMINARY; PRT; 134 AA.
 AC 09L657;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
 DE Histone-like nucleoid structuring protein.
 GN HNS.
 OS Proteus mirabilis.
 OC Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
 OC Proteus.
 OX NCBI_TaxID=584;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=H14320;
 RA Coker C., Bakare O.O., Mobley H.L.T.;
 RT "H-NS is a Repressor of the Proteus mirabilis Urease Transcriptional
 RT Activator Gene ureR";
 RL J. Bacteriol. 0:0-0(2000).
 DR EMBL; AF240693; AAF61240.1; -.
 DR HSSP; P08936; 1HNR.
 DR InterPro; IPR001801; Histone_HNS.
 DR Pfam; PF00816; Histone_HNS.1
 DR PRODOM; PD007337; Histone_HNS.1.
 DR SMART; SM00528; HNS.1.
 SQ SEQUENCE 134 AA; 15249 MW; 202C49BCA12597B3 CRC64;

Query Match 11.9%; Score 7; DB 2; Length 134;
 Best Local Similarity 100.0%; Pred. No. 9.6;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 28 KTGRAKR 34
 |||||
 Db 83 KTGRAKR 89

RESULT 15

09RSE5 PRELIMINARY; PRT; 154 AA.
 ID 09RSE5
 AC 09RSE5;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Hypothetical protein DR2179.
 GN DR2179.
 OS Deinococcus radiodurans.
 OC Bacteria; Thermus/Deinococcus group; Deinococci; Deinococcales;
 OC Deinococcaceae; Deinococcus.
 OX NCBI_TaxID=1299;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=RL;
 RX MEDLINE=20036896; PubMed=10567266;
 RA White O., Eisen J.A., Heidelberg J.F., Hickey E.K., Peterson J.D.,
 RA Dodson R.J., Haft D.H., Gwinn M.L., Nelson W.C., Richardson D.L.,
 RA Moffat K.S., Qin H., Jiang L., Pamphile W., Crosby M., Shen M.,
 RA Vamathevan J.J., Lam P., McDonald L., Uitterlinden T., Zaleski C.,
 RA Makarewicz K.S., Aravind L., Daly M.J., Minton K.W., Fleischmann R.D.,
 RA Ketchum K.A., Nelson K.E., Salzberg S., Smith R.O., Venter J.C.,
 RA Fraser C.M.;
 RT "Genome Sequence of the radioresistant bacterium Deinococcus
 RT radiodurans RL";
 RL Science 286:1571-1577(1999).
 DR EMBL; AE002051; AAF11732.1; -.
 DR TIGR; DR2179; -.
 KW Hypothetical protein; Complete proteome.
 SQ SEQUENCE 154 AA; 16181 MW; 58AA86884AA0D4C4 CRC64;

Query Match 11.9%; Score 7; DB 16; Length 154;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 RAGKVG 14
 |||||
 Db 39 RAGKVG 45

RESULT 16

09NBB4 PRELIMINARY; PRT; 157 AA.
 ID 09NBB4
 AC 09NBB4;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE Stretchin-MCK (Fragment).
 GN STRN-MCK OR CG8304 OR CG18255.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Champagne M.B., Edwards K.A., Erickson H.P., Kiehart D.P.;
 RT "Drosophila stretchin-MCK is a Novel Member of the Titin/Myosin Light
 RT Chain Kinase Family";
 RL J. Mol. Biol. 0:0-0(2000).
 DR EMBL; AF257306; AAF90124.1; -.
 DR FlyBase; FBgn0013986; Strn-MCK.
 FT NON_TER 1 157
 FT NON_TER 1 157
 SQ SEQUENCE 157 AA; 18077 MW; 0C73A2D3AE35278F CRC64;

Query Match 11.9%; Score 7; DB 5; Length 157;
 Best Local Similarity 100.0%; Pred. No. 11;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
 |||||
 Db 150 EKKKKKT 156

RESULT 17

09ZOB1 PRELIMINARY; PRT; 173 AA.
 ID 09ZOB1
 AC 09ZOB1;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-JUN-2002 (TREMBLrel. 21, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Putative DNA binding protein with homeobox domain.
 GN ATG36610.
 OS Arabidopsis thaliana (Mouse-ear cress).
 OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicotyledons; Rosidae;
 OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
 OX NCBI_TaxID=3702;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=CV. COLUMBIA.
 RA Lin X., Kaul S., Shea T.P., Fujii C.Y., Shen M., Vanaken S.E.,
 RA Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Benito M.-I.,
 RA Carreira A.J., Cressy T.H., Buell C.R., Town C.D., Nierman W.C.,
 RA Fraser C.M., Venter J.C.;
 RT Submitted (Feb-2002) to the EMBL/genbank/DBJ databases.
 DR EMBL; AC006282; AAD20137.2; -.
 DR EMBL; AC006919; AAM15313.1; -.
 KW DNA-binding; Homeobox; Nuclear protein.
 SQ SEQUENCE 173 AA; 20478 MW; 57A67DCDA47E75FF CRC64;

Query Match 11.9%; Score 7; DB 10; Length 173;
 Best Local Similarity 100.0%; Pred. No. 12;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 22 OEKKKKK 28
 |||||

Db 42 QEKKKK 48

RESULT 18

Q9AGU8 PRELIMINARY; PRT; 198 AA.
AC Q9AGU8;
DT 01-JUN-2001 (TReMBLrel. 17, Created)
DT 01-JUN-2001 (TReMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TReMBLrel. 21, Last annotation update)
DE Biotin carboxyl carrier protein (Fragment).
OS ACCB.
OS Brucella abortus.
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Brucellaceae; Brucella.
OX NCBI_TaxID=235;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=2308;
RA Essenberg R.C.;
RT "Cloning and sequence of the aroD gene of Brucella abortus.";
RL Submitted (DEC-2000) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF326476; AAK27449.1; -.
DR HSP: P02905; 3BD0.
DR InterPro: IPR001249; ACCOA_biotinCC.
DR InterPro: IPR001882; Biotin_attach.
DR InterPro: IPR000089; Biotin_11poyl.
DR Pfam: PF00364; Biotin_11poyl.1.
DR PRINTS: PR01071; AC0AB10TNC.
DR TIGRfams: TIGR00531; BCCP.1.
DR PROSITE: PS00188; BIOTIN; UNKNOWN_1.
FT NON_TER 198
SQ SEQUENCE 198 AA; 20832 MW; D6CB392BD4146F2 CRC64;

Query Match 11.9%; Score 7; DB 2; Length 198;
Best Local Similarity 100.0%; Pred. No. 14;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
IIIIIII
Db 40 KKKKKTG 46

RESULT 19

Q64075 PRELIMINARY; PRT; 215 AA.
AC Q64075;
DT 01-NOV-1996 (TReMBLrel. 01, Created)
DT 01-NOV-1996 (TReMBLrel. 01, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Nucleoporin p62 homolog protein (Fragment).
OS Rattus sp.
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10118;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=95151924; Pubmed=7849178;
RA Wang Z.Q., Akmal K.M., Kim K.H.;
RT "An unusual nucleoporin-related messenger ribonucleic acid is present in the germ cells of rat testis."
RL Biol. Reprod. 51:1022-1030(1994).
DR EMBL: S75997; AAB33384.1; -.
KW Porin.
FT NON_TER 1
SQ SEQUENCE 215 AA; 24593 MW; 098251C97A8FBD88 CRC64;

Query Match 11.9%; Score 7; DB 11; Length 215;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
IIIIIII

Db 52 KKKKKTG 58

RESULT 20

Q9LIR5 PRELIMINARY; PRT; 224 AA.
AC Q9LIR5;
DT 01-OCT-2000 (TReMBLrel. 15, Created)
DT 01-OCT-2000 (TReMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TReMBLrel. 19, Last annotation update)
DE Genomic DNA, chromosome 3, BAC clone:FL4013.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosid II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=COLUMBIA;
RA Kaneko T., Kato T., Sato S., Nakamura Y., Asamizu E., Tabata S.;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=20363099; Pubmed=10907853;
RA Nakamura Y.;
RT "Structural analysis of Arabidopsis thaliana chromosome 3. II. Sequence features of the regions of 4,251,695 bp covered by ninety P1, TAC and BAC clones."
RL DNA Res. 7:217-221(2000).
DR EMBL: AP001297; BAB03010.1; -.
SQ SEQUENCE 224 AA; 26999 MW; D4DFC32657C0A125 CRC64;

Query Match 11.9%; Score 7; DB 10; Length 224;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
IIIIIII
Db 200 KKKKKTG 206

RESULT 21

Q9FZ76 PRELIMINARY; PRT; 233 AA.
AC Q9FZ76;
DT 01-MAR-2001 (TReMBLrel. 16, Created)
DT 01-MAR-2001 (TReMBLrel. 16, Last sequence update)
DT 01-MAR-2002 (TReMBLrel. 20, Last annotation update)
DE Putative 60S ribosomal protein L6 (Putative 60S ribosomal protein L6).
GN F2516.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OX eurosids II; Brassicales; Brassicaceae; Arabidopsis.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RX Federerpiel N.A., Palm C.J., Conway A.B., Conn L., Hansen N.F., Altafi H., Nguyen M., Lam B., Southwick A., Miranda M., Brooks S., Buehler E., Chao O., Chin C., Chou J., Choi E., Gonzalez A., Hwang B., Johnson-Hopson C., Khan S., Kim C., Koo T., Lee J.M., Lenz C., Liu A., Liu S., Mukharisv N., Pham P., Sakano H., Shinn P., Toriumi M., Vaysberg M., Yu G., Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RX Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M., Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H., Cheuk K., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J., Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H., Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,

```
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (AUG-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RA Nguyen M., Karlin-Neumann G., Southwick A., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (JUN-2002) to the EMBL/GenBank/DBJ databases.
RN [3]
RA EMBL: AC062328; AAF98420.1; -
RA EMBL: AY054675; AAK96866.1; -
RA EMBL: AY072496; AAL66911.1; -
RA InterPro: IPR000915; Ribosomal_L6E.
RA Pfam: PF01159; Ribosomal_L6E; 1.
RA ProDom: PD009612; Ribosomal_L6E; 1.
RA Ribosomal protein.
SQ SEQUENCE 233 AA; 26153 MW; 1ED96B26A0F85CB CRC64;

Query Match 11.9%; Score 7; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
Db 166 EKKKKKT 172

RESULT 22
09C9C6 PRELIMINARY; PRT; 233 AA.
ID 09C9C6;
AC 09C9C6;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
DE Putative 60S ribosomal protein L6.
GN F2P9.7.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-CV. COLUMBIA;
RC MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dwar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Mafti R., Marshall A.,
RA Miltischer J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uteback T., Van Aken S., Vaysberg M., Vysotska V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana."
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
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RA Ecker J., Theologis A., Davis R.W.;
RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
RN [3]
RA EMBL: AC016662; AAG52524.1; -
RA EMBL: AY062622; AAL32700.1; -
RA InterPro: IPR000915; Ribosomal_L6E.
RA Pfam: PF01159; Ribosomal_L6E; 1.
RA ProDom: PD009612; Ribosomal_L6E; 1.
RA Ribosomal protein.
SQ SEQUENCE 233 AA; 26008 MW; 837890EFA8082A40 CRC64;

Query Match 11.9%; Score 7; DB 10; Length 233;
Best Local Similarity 100.0%; Pred. No. 16;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
Db 166 EKKKKKT 172

RESULT 23
09C9C5 PRELIMINARY; PRT; 233 AA.
ID 09C9C5;
AC 09C9C5;
DT 01-JUN-2001 (TrEMBLrel. 17, Created)
DT 01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
DE Putative 60S ribosomal protein L6.
GN F2P9.8 OR AT1G74050.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC SPRAIN-CV. COLUMBIA;
RC MEDLINE=21016719; PubMed=11130712;
RA Theologis A., Ecker J.R., Palm C.J., Federspiel N.A., Kaul S.,
RA White O., Alonso J., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,
RA Buehler E., Chan A., Chao Q., Chen H., Cheuk R.F., Chin C.W.,
RA Chung M.K., Conn L., Conway A.B., Conway A.R., Creasy T.H., Dwar K.,
RA Dunn P., Egu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,
RA Gill J.E., Goldsmith A.D., Haas B., Hansen N.F., Hughes B., Hultzer L.,
RA Hunter J.L., Jenkins J., Johnson-Hopson C., Khan S., Khaykin E.,
RA Kim C.J., Koo H.L., Kremetska I., Kurtz D.B., Kwan A., Lam B.,
RA Langin-Hooper S., Lee A., Lee J.M., Lenz C.A., Li J.H., Li Y.-P.,
RA Lin X., Liu S.X., Liu Z.A., Lueros J.S., Mafti R., Marshall A.,
RA Miltischer J., Miranda M., Nguyen M., Niernan W.C., Osborne B.I.,
RA Pal G., Peterson J., Pham P.K., Rizzo M., Rooney T., Rowley D.,
RA Sakano H., Salzberg S.L., Schwartz J.R., Shinn P., Southwick A.M.,
RA Sun H., Tallon L.J., Tambunga G., Toriumi M.J., Town C.D.,
RA Uteback T., Van Aken S., Vaysberg M., Vysotska V.S., Walker M.,
RA Wu D., Yu G., Fraser C.M., Venter J.C., Davis R.W.;
RA "Sequence and analysis of chromosome 1 of the plant Arabidopsis
RA thaliana."
RL Nature 408:816-820(2000).
RN [2]
RP SEQUENCE FROM N.A.
RA Southwick A., Karlin-Neumann G., Nguyen M., Lam B., Miranda M.,
RA Palm C.J., Bowser L., Jones T., Banh J., Carninci P., Chen H.,
RA Cheuk R., Chung M.K., Hayashizaki Y., Ishida J., Kamiya A., Kawai J.,
RA Kim C., Lin J., Liu S.X., Narusaka M., Pham P.K., Sakano H.,
RA Sakurai T., Satou M., Seki M., Shinn P., Yamada K., Shinozaki K.,
RA Ecker J., Theologis A., Davis R.W.;
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RL Submitted (FEB-2002) to the EMBL/GenBank/DBJ databases.

DR EMBL: AC016662; AAG52527.1; -
 DR EMBL: AY054573; AAG96764.1; -
 DR EMBL: AY081305; AAL91194.1; -
 DR InterPro: IPR000915; Ribosomal_L6E.
 DR Pfam: PF01159; Ribosomal_L6E; 1.
 DR ProDom: PD009612; Ribosomal_L6E; 1.
 KW Ribosomal protein.

SO SEQUENCE 233 AA; 26107 MW; 77268505F51280EA CRC64;

Query Match 11.9%; Score 7; DB 10; Length 233;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
 |||||
 DB 166 EKKKKKT 172

RESULT 24

09AD23 PRELIMINARY; PRT; 259 AA.

AC 09AD23;
 DT 01-JUN-2001 (TREMBLrel. 17, Created)
 DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Hypothetical protein SCPI.127.
 GN SCPI.127.
 OS Streptomyces coelicolor.
 OG Plasmid SCPI.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN=A3(2);
 RA Bentley S.D., Chater K.F., Cerdano-Tarraga A.-M., Challis G.L.,
 RA Thompson N.R., James K.D., Harris D.E., Quail M.A., Kieser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kieser T., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Barrell B.G., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete Streptomyces
 coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 DR EMBL: AL590463; CAC36648.1; -
 KW Hypothetical protein: Plasmid.
 SO SEQUENCE 259 AA; 28708 MW; 357BF1A6821CFE5F CRC64;

Query Match 11.9%; Score 7; DB 16; Length 259;
 Best Local Similarity 100.0%; Pred. No. 18;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 11
 |||||
 DB 127 SLARAG 133

RESULT 25

09NSK3 PRELIMINARY; PRT; 283 AA.

AC 09NSK3;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
 DE Hypothetical 31.4 kDa protein (Fragment).
 GN DKFZP621166.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MELANOMA;
 RA Bloecher H., Boecker M., Brandt P., Mewes H.W., Weil B., Wiemann S.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AL162072; CAB82408.1; -
 KW Hypothetical protein.
 FT NON_TER 1
 SO SEQUENCE 283 AA; 31436 MW; 3E3782A2086E9EE CRC64;

Query Match 11.9%; Score 7; DB 4; Length 283;
 Best Local Similarity 100.0%; Pred. No. 20;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSLARAG 10
 |||||
 DB 236 GSLARAG 242

RESULT 26

095T41 PRELIMINARY; PRT; 309 AA.

AC 095T41;
 DT 01-DEC-2001 (TREMBLrel. 19, Created)
 DT 01-DEC-2001 (TREMBLrel. 19, Last sequence update)
 DT 01-MAR-2002 (TREMBLrel. 20, Last annotation update)
 DE GH23743P.
 GN CG3441.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BERKELEY;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Farfan D., Frise E., George R.,
 RA Gonzalez M., Guarin H., Li P., Liao G., Miranda A., Mungall C.J.,
 RA Nuno J., Pacle J., Paragas V., Park S., Phouanavong S., Wan K.,
 RA Yu C., Lewis S.E., Rubin G.M., Celinker S.;
 RL Submitted (OCT-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY060340; AAL25379.1; -
 DR FLYBase: FBgn0035092; CG3441.
 SO SEQUENCE 309 AA; 34197 MW; 620BB8A464BEF487 CRC64;

Query Match 11.9%; Score 7; DB 5; Length 309;
 Best Local Similarity 100.0%; Pred. No. 21;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSLARAG 10
 |||||
 DB 153 GSLARAG 159

RESULT 27

066535 PRELIMINARY; PRT; 314 AA.

AC 066535;
 DT 01-AUG-1998 (TREMBLrel. 07, Created)
 DT 01-AUG-1998 (TREMBLrel. 07, Last sequence update)
 DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
 DE Riboflavin kinase.
 GN RIBF OR AO.139.
 OS Aquifex aeolicus.
 OC Bacteria; Aquificae; Aquificales; Aquificaceae; Aquifex.
 RN NCBI_TaxID=63363;
 RP SEQUENCE FROM N.A.
 RC STRAIN=VF5;
 RX MEDLINE=98196666; PubMed=9537320;
 RA Deckert G., Warren P.V., Gaasterland T., Young W.G., Lenox A.L.,

RA Graham D.E., Overbeek R., Sneed M.A., Keller M., Anujay M., Huber R.,
 RA Feldman R.A., Short J.M., Olson G.J., Swanson R.V.;
 RT "The complete genome of the hyperthermophilic bacterium Aquifex
 RT aeolicus";
 RL Nature 392:353-358(1998).
 DR EMBL: AE000675; AAC06488.1; -;
 DR InterPro: IPR002606; FAD_Synth.
 DR Pfam: PF01687; FAD_Synth. 1.
 DR ProDom: PD003662; FAD_Synth. 1.
 DR TIGRFAMs: TIGR00083; rldf. 1.
 KM Complete proteome.
 SQ SEQUENCE 314 AA; 36660 MW; 81F8B09671CE70E5 CRC64;

Query Match 11.9%; Score 7; DB 16; Length 314;
 Best Local Similarity 100.0%; Pred. No. 22;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 47 PTFGKKK 53
 DB 253 PTFGKKK 259

RESULT 28
 ID 095XC7 PRELIMINARY; PRT; 339 AA.
 AC 095XC7;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Hypothetical 37.3 kDa protein.
 GN Y338BL.31.
 OS Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 OC Rhabditidae; Peloderinae; Caenorhabditis.
 OX NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RX MEDLINE=99069613; PubMed=9851916;
 RA None;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Graves T.;
 RT "The sequence of C. elegans cosmid Y338BL.";
 RL Submitted (OCT-2000) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BRISTOL N2;
 RA Waterston R.;
 RT "Direct Submission.";
 RL Submitted (NOV-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC0084197; AAL00874.2; -;
 DR InterPro: IPR000620; DUF6. 1.
 DR Pfam: PF00892; DUF6. 1.
 KM Hypothetical protein.
 SQ SEQUENCE 339 AA; 37344 MW; 6793E7D389006C31 CRC64;

Query Match 11.9%; Score 7; DB 5; Length 339;
 Best Local Similarity 100.0%; Pred. No. 23;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 48 TFGKKK 54
 DB 91 TFGKKK 97

RESULT 29
 ID 096GN4 PRELIMINARY; PRT; 380 AA.

AC 096GN4;
 DT 01-DEC-2001 (Tremblrel. 19, Created)
 DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
 DT 01-MAR-2002 (Tremblrel. 20, Last annotation update)
 DE Similar to kinesin family member 5B.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Euteria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-B-CELL;
 RA Strausberg R.;
 RL Submitted (JUN-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC009353; AAH09353.1; -;
 DR InterPro: IPR001752; kinesin_motor.
 DR Pfam: PF00225; kinesin. 1.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN_1.
 DR PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KM ATP-binding; Coiled coil; Microtubules; Motor protein.
 SQ SEQUENCE 380 AA; 43059 MW; 912B4E7371C23650 CRC64;

Query Match 11.9%; Score 7; DB 4; Length 380;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
 DB 345 EKKKKKT 351

RESULT 30
 ID 09W0W6 PRELIMINARY; PRT; 380 AA.
 AC 09W0W6;
 DT 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
 DT 01-MAY-2000 (Tremblrel. 13, Last annotation update)
 DE CG3441 protein.
 GN CG3441.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Insecta;
 OC Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OX NCBI_TaxID=7227;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-BERKELEY;
 RX MEDLINE=20196006; PubMed=10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner S., Henderson S.N.,
 RA Sultion G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H.C., Blazey R.G., Champe M., Pfeiffer B.D.,
 Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Mills G.L.G.,
 RA Abril J.F., Abdayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos R., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster A., Gabrielian A.E., Gang N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketcho K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Stimpson M., Skupski M.P., Smith T.,
 RA Slier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.-Y., Massarman D.A., Weinstein G.M., Weissenbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A.,
 RA Ye J., Yeh R.-F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gidbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 DR EMBL: AEO03466; AAF47313.1; -;
 DR Flybase: FBgn0035092; CG3441.
 SO SEQUENCE 380 AA; 41734 MW; 35722F8707289C3F CRC64;

Query Match 11.9%; Score 7; DB 5; Length 380;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSLARAG 10
 DB 153 GSLARAG 159

RESULT 31
 Q15694 PRELIMINARY; PRT; 381 AA.
 AC Q15694;
 DT 01-NOV-1996 (TrEMBLrel. 01, Created)
 DT 01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
 DT 01-NOV-1998 (TrEMBLrel. 08, Last annotation update)
 DE Protein immuno-reactive with anti-PTH polyclonal antibodies
 OS (Fragment).
 DE Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-96187433; Pubmed-8608414;
 RA Kumar R., Haugen J.D., Wieben E.D., Londowski J.M., Cai Q.;
 RT "Inhibitors of renal epithelial phosphate transport in tumor-induced
 RL osteomalacia and uremia.";
 RT Proc. Assoc. Am. Physicians 107:296-305(1995).
 DR EMBL: U28831; AAB02177.1; -;
 FT NON_TER 1
 FT NON_TER 381
 SO SEQUENCE 381 AA; 42574 MW; BFE144AB3A21C6DD CRC64;

Query Match 11.9%; Score 7; DB 4; Length 381;
 Best Local Similarity 100.0%; Pred. No. 26;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 QEKKKK 28
 DB 375 QEKKKK 381

RESULT 32
 Q9S2F0 PRELIMINARY; PRT; 424 AA.
 AC Q9S2F0;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Putative ABC transporter ATP-binding protein.
 GN SCO2931 OR SCE19A.31.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.

OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA Seeger K., Harris D.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RA James K.D., Parkhill J., Barrell B.G., Rajandream M.A.;
 RL Submitted (JUL-1999) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2);
 RX MEDLINE-97000351; Pubmed-8843436;
 RA Redenbach M., Kleser H.M., Denapalte D., Eichner A., Cullum J.,
 RA Kinashi H., Hopwood D.A.;
 RT "A set of ordered cosmids and a detailed genetic and physical map for
 RL the 8 Mb streptomyces coelicolor A3(2) chromosome.";
 RL Mol. Microbiol. 21:77-96(1996).
 RN [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN-A3(2) / M145;
 RA Bentley S.D., Chater K.F., Cerdeno-Tarraga A.-M., Challis G.L.,
 RA Thomson N.R., James K.D., Harris D.E., Quail M.A., Kleser H.,
 RA Harper D., Bateman A., Brown S., Chandra G., Chen C.W., Collins M.,
 RA Cronin A., Fraser A., Goble A., Hidalgo J., Hornsby T., Howarth S.,
 RA Huang C.-H., Kleser I., Larke L., Murphy L., Oliver K., O'Neill S.,
 RA Rabinowitsch E., Rajandream M.A., Rutherford K., Rutter S.,
 RA Seeger K., Saunders D., Sharp S., Squares R., Squares S., Taylor K.,
 RA Warren T., Wietzorrek A., Woodward J., Parkhill J.,
 RA Hopwood D.A.;
 RT "Complete genome sequence of the model actinomycete *Streptomyces*
 RL coelicolor A3(2).";
 RL Nature 417:141-147(2002).
 CC -1- SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AL096852; CAB51012.1; -;
 DR InterPro: IPR003593; AAA_ATPase.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR000644; CBS_domain.
 DR Pfam: PF00005; ABC_tran; 1.
 DR Pfam: PF00571; CBS; 2.
 DR ProDom: PD000006; ABC_transport; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRfams: TIGR01186; prov; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport.
 KW SEQUENCE 424 AA; 46529 MW; BE6BBD3D89BFF1E CRC64;

Query Match 11.9%; Score 7; DB 16; Length 424;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSLARAG 10
 DB 328 GSLARAG 334

RESULT 33
 Q9X4J1 PRELIMINARY; PRT; 429 AA.
 AC Q9X4J1;
 DT 01-NOV-1999 (TrEMBLrel. 12, Created)
 DT 01-NOV-1999 (TrEMBLrel. 12, Last sequence update)
 DT 01-JUN-2002 (TrEMBLrel. 21, Last annotation update)
 DE Provl.
 GN PROVL.
 OS Streptomyces coelicolor.
 OC Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
 OC Actinomycetales; Streptomycinae; Streptomycetaceae; Streptomyces.
 OX NCBI_TaxID=1902;
 RN [1]
 RP SEQUENCE FROM N.A.

RC STRAIN-M145;
 RA Tan H., Tian Y., Yang H., Chater K.F.;
 RT "Study on a proU-like operon which related to glycine-betaine
 transport of *Streptomyces coelicolor*";
 RL Submitted (DEC-1998) to the EMBL/Genbank/DBJ databases.
 CC -1. SIMILARITY: BELONGS TO THE ABC TRANSPORTER FAMILY.
 DR EMBL: AF112365; AAD29279.1; -.
 DR InterPro: IPR003593; AAA_Atpase.
 DR InterPro: IPR003439; ABC_transport.
 DR InterPro: IPR000644; CBS_domain.
 DR Pfam: PF000571; ABC_tran; 1.
 DR ProDom: PD000006; ABC_transport; 1.
 DR SMART: SM00382; AAA; 1.
 DR TIGRFAMs: TIGR01186; proV; 1.
 DR PROSITE: PS00211; ABC_TRANSPORTER; 1.
 KW ATP-binding; Transport.
 SQ SEQUENCE 429 AA; 47360 MW; 9053661CAB5A4484 CRC64;

Query Match 11.9%; Score 7; DB 2; Length 429;
 Best Local Similarity 100.0%; Pred. No. 29;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSIRAG 10
 DB 333 GSIRAG 339

RESULT 34
 O9K509 PRELIMINARY; PRT; 454 AA.
 AC O9K509;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2002 (TREMBlrel. 21, Last annotation update)
 DE Replicative DNA helicase.
 GN DMC OR BH4029.
 OS *Bacillus halodurans*.
 OC Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillales;
 OC Bacillaceae; Bacillus.
 OX NCBI_Taxid=86665;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C-125 / JCM 9153;
 RX MEDLINE=20512582; PubMed=11058132;
 RA Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R., Masui N.,
 RA Fujii F., Hirama C., Nakamura Y., Ogasawara N., Kuhara S.,
 RA Horikoshi K.;
 RT "Complete genome sequence of the alkaliphilic bacterium *Bacillus*
 RT *halodurans* and genomic sequence comparison with *Bacillus subtilis*.";
 RL Nucleic Acids Res. 28:4317-4331(2000).
 DR EMBL: AP001520; BAB07748.1; -.
 DR HSSP: P03005; LWE.
 DR InterPro: IPR001198; DnaB_helicase.
 DR Pfam: PF00772; DnaB; 1.
 DR TIGRFAMs: TIGR00065; DnaB; 1.
 KW Helicase; Complete proteome.
 SQ SEQUENCE 454 AA; 50630 MW; D9D6DE17A52EAD3A CRC64;

Query Match 11.9%; Score 7; DB 16; Length 454;
 Best Local Similarity 100.0%; Pred. No. 31;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 4 GSIRAG 10
 DB 281 GSIRAG 287

RESULT 35
 O91290 PRELIMINARY; PRT; 542 AA.
 AC O91290;
 DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-DEC-2001 (TREMBlrel. 19, Last annotation update)
 DE Heat shock protein 90 (Fragment).
 GN HSC90.
 OS *Plutodelles waltiti* (Iberian ribbed newt).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Caudata; Salamandroidea; Salamandridae;
 OC *Plutodelles*.
 OX NCBI_Taxid=8319;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=95246904; PubMed=7729567;
 RA Courailleau P., Billoud B., Sourrouille P., Moreau N., Angelier N.;
 RT "Evidence for a 90 kDa heat-shock protein gene expression in the
 RT amphibian oocyte.";
 RL Dev. Biol. 168:247-258(1995).
 DR EMBL: U32987; AAA92343.1; -.
 DR HSSP: P07900; 1YER.
 DR InterPro: IPR001404; Hsp90.
 DR Pfam: PF00183; HSP90; 1.
 KW NON_TER
 SQ SEQUENCE 542 AA; 63096 MW; E2FAEAB9250C2626 CRC64;

Query Match 11.9%; Score 7; DB 13; Length 542;
 Best Local Similarity 100.0%; Pred. No. 37;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKKKT 29
 DB 81 EKKKKKT 87

RESULT 36
 O9NXU4 PRELIMINARY; PRT; 576 AA.
 AC O9NXU4;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-MAR-2002 (TREMBlrel. 20, Last annotation update)
 DE CDNA FLJ20052 fis, clone COL00777 (Fragment).
 OS *Homo sapiens* (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=COLON;
 RA Kawabata A., Hiki J. T., Kobatake N., Inagaki H., Ikema Y., Okamoto S.,
 RA Okitani R., Ota T., Suzuki Y., Odayashi M., Nishi T., Shibahara T.,
 RA Tanaka T., Nakamura Y., Isegaki T., Sugano S.;
 RT "NEDO human cDNA sequencing project.";
 RL Submitted (FEB-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL: AK000059; BAA90916.1; -.
 DR HSSP: P17119; 3KAR.
 DR InterPro: IPR001752; kinesin_motor.
 DR Pfam: PF00225; kinesin; 1.
 DR PRINTS: PR00380; KINESINHEAVY.
 DR SMART: SM00129; KISC; 1.
 DR PROSITE: PS00411; KINESIN_MOTOR_DOMAIN1; UNKNOWN; 1.
 KW PROSITE: PS50067; KINESIN_MOTOR_DOMAIN2; 1.
 KW ATP-binding; Coiled coil; Microtubules; Motor protein.
 KW NON_TER
 SQ SEQUENCE 576 AA; 64518 MW; A21BBE950F4946D6 CRC64;

Query Match 11.9%; Score 7; DB 4; Length 576;
 Best Local Similarity 100.0%; Pred. No. 39;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKKK 28
 DB 570 OEKKKKK 576

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RESULT 37
098CL9 PRELIMINARY: PRT: 594 AA.
AC 098CL9:
DT 01-OCT-2001 (TREMBLrel. 18, Created)
DT 01-OCT-2001 (TREMBLrel. 18, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Two-component sensor histidine kinase, Exos.
GN MLL5094.
OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.
OX NCBI_TaxID=381;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=MAF303099;
RX MEDLINE=21082930; PubMed=11214968;
RA Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasamoto S.,
RA Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura T.,
RA Kishida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A.,
RA Mochizuki Y., Nakayama S., Nakazaki N., Shimo S., Sugimoto M.,
RA Takeuchi C., Yamada M., Tabeta S.;
RT "Complete genome structure of the nitrogen-fixing symbiotic bacterium
RT Mesorhizobium loti."
RL DNA Res. 7:331-338(2000).
DR EMBL: AP003005; BAB51602.1; -.
DR InterPro: IPR003594; ATPbind_ATPase.
DR InterPro: IPR004358; Bact_sens_Pt_C.
DR InterPro: IPR003660; HAMp.
DR InterPro: IPR003661; His_kinA.
DR InterPro: IPR004359; His_Kin_slg.
DR Pfam: PF00672; HAMp_1.
DR Pfam: PF02518; HAMpase_C_1.
DR Pfam: PF00512; signal_1.
DR PRINTS: PR00344; BCTRSENSOR.
DR SMART: SM00304; HAMp_1.
DR SMART: SM00387; HAMpase_C_1.
DR SMART: SM00388; HlsK_1.
KW kinase: Complete proteome.
SQ SEQUENCE 594 AA; 65169 MW; EDE20CFA78D72819 CRC64;

Query Match 11.9%; Score 7; DB 16; Length 594;
Best Local Similarity 100.0%; Pred. No. 40;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARACK 11
DB 505 SLARACK 511

RESULT 38
09M8T5 PRELIMINARY: PRT: 806 AA.
AC 09M8T5:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-DEC-2001 (TREMBLrel. 19, Last annotation update)
DE F13E7.12 protein.
GN F13E7.12.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. COLUMBIA;
RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B., Wu D.,
RA Bonning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
RT "Arabidopsis thaliana chromosome III BAC F13E7 genomic sequence.";
RT Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: AC018363; AAF26966.1; -.

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DR InterPro: IPR000875; Cecropin.
DR InterPro: IPR000533; Tropomyosin.
DR PRINTS: PR00194; TROPOMYOSIN.
DR PROSITE: PS00268; CECROPIN; UNKNOWN_1.
SQ SEQUENCE 806 AA; 91859 MW; AFE6F9AED5D4BFD CRC64;

Query Match 11.9%; Score 7; DB 10; Length 806;
Best Local Similarity 100.0%; Pred. No. 53;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKKKT 29
DB 782 EKKKKKT 788

RESULT 39
09M0D8 PRELIMINARY: PRT: 863 AA.
AC 09M0D8:
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DT 01-JUN-2002 (TREMBLrel. 21, Last annotation update)
DE Serine/threonine-specific receptor protein kinase-1like protein.
GN AT4G29450.
OS Arabidopsis thaliana (Mouse-ear cress).
OC Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
OC Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
OC eurosids II; Brassicales; Brassicaceae; Arabidopsids.
OX NCBI_TaxID=3702;
RN [1]
RP SEQUENCE FROM N.A.
RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,
RA Mewes H.W., Lemcke K., Mayer K.F.X.;
RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
RL [2]
RP SEQUENCE FROM N.A.
RA EU Arabidopsis sequencing project;
RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
DR EMBL: AL161575; CAB79703.1; -.
DR InterPro: IPR00719; Euk_pkinase.
DR InterPro: IPR002896; Herpes_glycop_D.
DR InterPro: IPR001611; LRR.
DR InterPro: IPR003592; LRR_out.
DR InterPro: IPR002290; Ser_thr_pkinase.
DR InterPro: IPR004040; STY_pkinase.
DR InterPro: IPR001245; TYR_pkinase.
DR Pfam: PF01537; Herpes_glycop_D; 1.
DR Pfam: PF00560; LRR; 2.
DR Pfam: PF00069; pkinase; 1.
DR PRINTS: PR01651; SECSEXPORT.
DR PRINTS: PR00109; TYRKINASE.
DR PRODOM: PD000001; Euk_pkinase; 1.
DR SMART: SM00370; LRR; 2.
DR SMART: SM00221; STYKc; 1.
DR PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.
DR PROSITE: PS50011; PROTEIN_KINASE_DOM; 1.
DR PROSITE: PS00108; PROTEIN_KINASE_ST; 1.
KW ATP-binding; Kinase; Receptor; Serine/threonine-protein kinase;
KW Transferrase.
SQ SEQUENCE 863 AA; 96557 MW; 32AE253F9C708427 CRC64;

Query Match 11.9%; Score 7; DB 10; Length 863;
Best Local Similarity 100.0%; Pred. No. 57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 22 QEKKKKK 28
DB 504 QEKKKKK 510

RESULT 40
09MC26

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ID 09WC26 PRELIMINARY; PRT; 1254 AA.
AC 09WC26;
DT 01-NOV-1999 (TREMblrel. 12, Created)
DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Structural polypeptide.
OS Venezuelan equine encephalitis virus (strain Mena II).
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=36384;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-MENA II;
RA MEDLINE-99101297; PubMed-9886206;
RA Kinney R.M., Pfeffer M., Tsuchiya K.R., Chang G.J., Roehrig J.F.;
RT "Nucleotide sequences of the 26S mRNAs of the viruses defining the
RT Venezuelan equine encephalitis antigenic complex.";
RL Am. J. Trop. Med. Hyg. 59:952-964(1998).
RM [2]
RP SEQUENCE FROM N.A.
RC STRAIN-MENA II;
RA Kinney R.M., Pfeffer M., Weissner J.;
RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL; AF075252; AAD14553.1; -.
DR HSSP; P03315; 1VCP.
DR InterPro; IPR001836; Alpha_core.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000936; Alpha_E2_glycop.
DR InterPro; IPR002533; Alpha_E3_glycop.
DR InterPro; IPR000930; Togavirin.
DR Pfam; PF00944; Alpha_core; 1.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Polypeptide.
FT CHAIN 1 274 NUCLEOCAPSID PROTEIN.
FT CHAIN 275 333 POLYPEPTIDE CLEAVAGE PRODUCT E3.
FT CHAIN 334 756 ENVELOPE GLYCOPROTEIN 2.
FT CHAIN 757 812 6K POLYPEPTIDE CLEAVAGE PRODUCT.
FT CHAIN 813 1254 ENVELOPE GLYCOPROTEIN 1.
SQ SEQUENCE 1254 AA; 138329 MW; 0E3321D41F4DEB39 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKRTG 30
Db 88 KKKKRTG 94

RESULT 41
O9YKD3 PRELIMINARY; PRT; 1254 AA.
AC O9YKD3;
DT 01-MAY-1999 (TREMblrel. 10, Created)
DT 01-MAY-1999 (TREMblrel. 10, Last sequence update)
DT 01-MAR-2002 (TREMblrel. 20, Last annotation update)
DE Structural polypeptide.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE-96347778; PubMed-9684636;
RA Oberste M.S., Fraile M., Navarro R., Zepeda C., Zarate M.L.,
RA Ludwig G.V., Kondig J.F., Weaver S.C., Smith J.F., Rico-Hesse R.;
RT "Association of Venezuelan equine encephalitis virus subtype IE with
RT two equine epizootics in Mexico.";
RL Am. J. Trop. Med. Hyg. 59:100-107(1998).
RM [2]
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RP SEQUENCE FROM N.A.
RC STRAIN-OAX142;
RX MEDLINE-21657447; PubMed-11799167;
RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
RT "Positively charged amino acid substitutions in the E2 envelope
RT glycoprotein are associated with the emergence of Venezuelan equine
RT encephalitis virus.";
RL J. Virol. 76:1718-1730(2002).
DR EMBL; U96408; AAD19216.1; -.
DR EMBL; AF448538; AAL47153.1; -.
DR HSSP; P03315; 1VCP.
DR MEROPS; S03.001; -.
DR InterPro; IPR001836; Alpha_core.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000936; Alpha_E2_glycop.
DR InterPro; IPR002533; Alpha_E3_glycop.
DR InterPro; IPR000930; Togavirin.
DR Pfam; PF00944; Alpha_core; 1.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Polypeptide.
SQ SEQUENCE 1254 AA; 138377 MW; C07D6844531DA587 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKRTG 30
Db 88 KKKKRTG 94

RESULT 42
O88979 PRELIMINARY; PRT; 1254 AA.
AC O88979;
DT 01-NOV-1996 (TREMblrel. 01, Created)
DT 01-NOV-1996 (TREMblrel. 01, Last sequence update)
DT 01-DEC-2001 (TREMblrel. 19, Last annotation update)
DE Structural polypeptide.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage; Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-680201;
RX MEDLINE-96204604; PubMed-8623548;
RA Oberste M.S., Parker M.D., Smith J.F.;
RT "Complete sequence of Venezuelan equine encephalitis virus subtype IE
RT reveals conserved and hypervariable domains within the C terminus of
RT nsP3.";
RL Virology 219:314-320(1996).
DR EMBL; U34999; AAB04683.1; -.
DR HSSP; P03315; 1VCP.
DR InterPro; IPR001836; Alpha_core.
DR InterPro; IPR002548; Alpha_E1_glycop.
DR InterPro; IPR000936; Alpha_E2_glycop.
DR InterPro; IPR002533; Alpha_E3_glycop.
DR InterPro; IPR000930; Togavirin.
DR Pfam; PF00944; Alpha_core; 1.
DR Pfam; PF01589; Alpha_E1_glycop; 1.
DR Pfam; PF00943; Alpha_E2_glycop; 1.
DR Pfam; PF01563; Alpha_E3_glycop; 1.
DR PRINTS; PR00798; TOGAVIRIN.
KW Polypeptide.
SQ SEQUENCE 1254 AA; 138258 MW; BFFB9F3BD6C99C1 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 24 KKKKKTG 30
      |||||
DB 88 KKKKKTG 94

RESULT 43
08V293
ID 08V293 PRELIMINARY; PRT: 1254 AA.
AC 08V293;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Structural polyprotein.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage: Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC MEDLINE=21657447; PubMed=11799167;
RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
RT "Positively charged amino acid substitutions in the E2 envelope
RT glycoprotein are associated with the emergence of Venezuelan equine
RT encephalitis virus."
RL J. Virol. 76:1718-1730(2002).
DR EMBL: AF448537; AAL47151.1; -.
DR InterPro: IPR001836; Alpha_E1-glycop.
DR InterPro: IPR002548; Alpha_E1-glycop.
DR InterPro: IPR000936; Alpha_E2-glycop.
DR InterPro: IPR002533; Alpha_E3-glycop.
DR InterPro: IPR000930; Togavirin.
DR Pfam: PF00944; Alpha_Core; 1.
DR Pfam: PF01589; Alpha_E1-glycop; 1.
DR Pfam: PF00943; Alpha_E2-glycop; 1.
DR Pfam: PF01563; Alpha_E3-glycop; 1.
DR PRINTS: PR00798; TOGAVIRIN.
KW Polyprotein.
SQ SEQUENCE 1254 AA; 138376 MW; E024103E7F6B0FD4 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
      |||||
DB 88 KKKKKTG 94

RESULT 44
08V291
ID 08V291 PRELIMINARY; PRT: 1254 AA.
AC 08V291;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Structural polyprotein.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage: Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=80076;
RX MEDLINE=21657447; PubMed=11799167;
RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
RT "Positively charged amino acid substitutions in the E2 envelope
RT glycoprotein are associated with the emergence of Venezuelan equine
RT encephalitis virus."
RL J. Virol. 76:1718-1730(2002).
DR EMBL: AF448539; AAL47155.1; -.
DR InterPro: IPR001836; Alpha_Core.
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DR InterPro: IPR002548; Alpha_E1-glycop.
DR InterPro: IPR000936; Alpha_E2-glycop.
DR InterPro: IPR002533; Alpha_E3-glycop.
DR InterPro: IPR000930; Togavirin.
DR Pfam: PF00944; Alpha_Core; 1.
DR Pfam: PF01589; Alpha_E1-glycop; 1.
DR Pfam: PF00943; Alpha_E2-glycop; 1.
DR Pfam: PF01563; Alpha_E3-glycop; 1.
DR PRINTS: PR00798; TOGAVIRIN.
KW Polyprotein.
SQ SEQUENCE 1254 AA; 138341 MW; 6EC946B80BEA6817 CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1254;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
      |||||
DB 88 KKKKKTG 94

RESULT 45
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ID 08VYH1 PRELIMINARY; PRT: 1264 AA.
AC 08VYH1;
DT 01-MAR-2002 (Tremblrel. 20, Created)
DT 01-MAR-2002 (Tremblrel. 20, Last sequence update)
DE 01-JUN-2002 (Tremblrel. 21, Last annotation update)
DE Structural polyprotein.
OS Venezuelan equine encephalitis virus.
OC Viruses; ssRNA positive-strand viruses, no DNA stage: Togaviridae;
OC Alphavirus.
OX NCBI_TaxID=11036;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=OAX131, AND CPA152;
RX MEDLINE=21657447; PubMed=11799167;
RA Brault A.C., Powers A.M., Holmes E.C., Woelk C.H., Weaver S.C.;
RT "Positively charged amino acid substitutions in the E2 envelope
RT glycoprotein are associated with the emergence of Venezuelan equine
RT encephalitis virus."
RL J. Virol. 76:1718-1730(2002).
DR EMBL: AF448536; AAL47149.1; -.
DR EMBL: AF448535; AAL47147.1; -.
DR InterPro: IPR001836; Alpha_Core.
DR InterPro: IPR002548; Alpha_E1-glycop.
DR InterPro: IPR000936; Alpha_E2-glycop.
DR InterPro: IPR002533; Alpha_E3-glycop.
DR InterPro: IPR000930; Togavirin.
DR Pfam: PF00944; Alpha_Core; 1.
DR Pfam: PF01589; Alpha_E1-glycop; 1.
DR Pfam: PF00943; Alpha_E2-glycop; 1.
DR Pfam: PF01563; Alpha_E3-glycop; 1.
DR PRINTS: PR00798; TOGAVIRIN.
KW Polyprotein.
SQ SEQUENCE 1264 AA; 139454 MW; 39DBF657BDADF7F CRC64;

Query Match 11.9%; Score 7; DB 12; Length 1264;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKTG 30
      |||||
DB 98 KKKKKTG 104
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Search completed: February 6, 2003, 21:31:48
Job time : 33 secs

GenCore version 5.1.3
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OM protein - protein search, using sw model

Run on: February 6, 2003, 21:30:59 : Search time 15 Seconds
(without alignments)
115.730 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KKHSLARAGKVRGQTPKVA.....RRFVVVPTFGKKKGNMNS 59

Scoring table: OLIGO

Gapop 60.0 , Gapept 60.0

Searched: 262574 seqs, 29422922 residues

Word size : 0

Total number of hits satisfying chosen parameters: 262574

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

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- 2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/5A_COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/5B_COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PCTUS_COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	11.9	381	1	US-08-487-810-2
2	7	11.9	409	2	US-08-743-130A-2
3	7	11.9	409	2	US-08-743-130A-39
4	7	11.9	7257	3	US-09-335-409-5
5	7	11.9	7257	4	US-09-568-102-5
6	7	11.9	7257	4	US-09-567-969-5
7	7	11.9	7257	4	US-09-568-480-5
8	7	11.9	7257	4	US-09-568-486-5
9	7	11.9	7257	4	US-09-568-472-5
10	7	11.9	7257	4	US-09-567-899-5
11	6	10.2	15	4	US-09-082-358B-24
12	6	10.2	15	4	US-09-082-358B-62
13	6	10.2	15	3	US-08-851-843A-201
14	6	10.2	16	4	US-08-974-549A-330
15	6	10.2	16	4	US-08-854-050-201
16	6	10.2	16	4	US-08-854-050-201
17	6	10.2	16	4	US-09-430-323-201
18	6	10.2	29	4	US-09-177-249-189
19	6	10.2	51	4	US-09-227-357-479
20	6	10.2	55	4	US-08-569-749-5
21	6	10.2	55	5	PCT-US96-12860-5
22	6	10.2	55	5	PCT-US96-12860-5
23	6	10.2	57	4	US-09-082-358B-43
24	6	10.2	63	4	US-08-971-089-2
25	6	10.2	68	2	US-08-511-485-18
26	6	10.2	68	2	US-08-511-485-19
27	6	10.2	141	4	US-09-091-725-51

28	6	10.2	154	4	US-08-871-732A-1	Sequence 1, Appl1
29	6	10.2	154	4	US-09-346-510B-1	Sequence 1, Appl1
30	6	10.2	175	2	US-08-533-669A-4	Sequence 4, Appl1
31	6	10.2	175	4	US-09-183-861-4	Sequence 4, Appl1
32	6	10.2	197	1	US-09-022-765-4	Sequence 4, Appl1
33	6	10.2	197	1	US-08-468-347-24	Sequence 24, Appl1
34	6	10.2	197	2	US-08-467-389-24	Sequence 24, Appl1
35	6	10.2	197	2	US-08-779-379-24	Sequence 24, Appl1
36	6	10.2	197	2	US-08-469-219-24	Sequence 24, Appl1
37	6	10.2	197	2	US-09-228-152-24	Sequence 24, Appl1
38	6	10.2	234	4	US-08-903-801-3	Sequence 3, Appl1
39	6	10.2	234	4	US-09-295-055-3	Sequence 3, Appl1
40	6	10.2	251	4	US-09-149-476-568	Sequence 568, App
41	6	10.2	316	4	US-09-347-803-20	Sequence 20, Appl1
42	6	10.2	318	4	US-09-615-192A-389	Sequence 389, App
43	6	10.2	341	4	US-09-347-803-16	Sequence 16, Appl1
44	6	10.2	370	2	US-08-729-214-27	Sequence 27, Appl1
45	6	10.2	370	3	US-09-028-934-27	Sequence 27, Appl1

ALIGNMENTS

```
RESULT 1
US-08-487-810-2
; Sequence 2, Application US/08487810
; Patent No. 5618695
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: DNA ENCODING HEM-1, A GENE EXPRESSED BY
; TITLE OF INVENTION: SCLEROSING HEMANGIOMA CELLS
; NUMBER OF SEQUENCES: 2
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/487,810
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 381 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-487-810-2

Query Match      11.9% Score 7; DB 1;
Best Local Similarity 100.0%; Pred. No. 8.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 22 OEKKKK 28
Db 375 OEKKKK 381

RESULT 2
US-08-743-130A-2
; Sequence 2, Application US/08743130A
; Patent No. 5871987
; GENERAL INFORMATION:
; APPLICANT: Sasanifar, Mandana
; APPLICANT: Gallant, Paul L.
; APPLICANT: Shen, Xiaoyu
; APPLICANT: Tao, Nianjun
; APPLICANT: Tao, Jianshi
; APPLICANT: Houman, Fariba
; TITLE OF INVENTION: CANDIDA TYROSYL-tRNA SYNTHETASE
; TITLE OF INVENTION: PROTEINS, NUCLEIC ACIDS AND STRAINS COMPRISING SAME
; NUMBER OF SEQUENCES: 41
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P.C.
```

STREET: Two Millitia Drive
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI95-12
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-743-130A-2
MOLECULE TYPE: protein

Query Match 11.9%; Score 7; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KOEKKK 27
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DB 360 KOEKKK 366

RESULT 3
US-08-743-130A-39
Sequence 39, Application US/08743130A
Patent No. 5871987
GENERAL INFORMATION:
APPLICANT: Sassanfar, Mandana
APPLICANT: Gallant, Paul L.
APPLICANT: Shen, Xiaoyu
APPLICANT: Tao, Nianjun
APPLICANT: Tao, Jianshi
APPLICANT: Houman, Fariba
TITLE OF INVENTION: CANDIDA TYROSYL-TRNA SYNTHETASE
NUMBER OF INVENTION: 41
NUMBER OF SEQUENCES: 41
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hamilton, Brook, Smith & Reynolds, P. C.
CITY: Lexington
STATE: Massachusetts
COUNTRY: USA
ZIP: 02173
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentln Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/743,130A
FILING DATE: 01-NOV-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Brook Esq., David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CPI95-12

TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 861-6240
TELEFAX: (617) 861-9540
INFORMATION FOR SEQ ID NO: 39:
SEQUENCE CHARACTERISTICS:
LENGTH: 409 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-08-743-130A-39

Query Match 11.9%; Score 7; DB 2; Length 409;
Best Local Similarity 100.0%; Pred. No. 9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 21 KOEKKK 27
|||||
DB 360 KOEKKK 366

RESULT 4
US-09-335-409-5
Sequence 5, Application US/09335409
Patent No. 6121029
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/335,409
CURRENT FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-335-409-5

Query Match 11.9%; Score 7; DB 3; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 STARAK 11
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DB 7250 STARAK 7256

RESULT 5
US-09-568-102-5
Sequence 5, Application US/09568102
Patent No. 6346404
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,102
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentln Ver. 2.0
SEQ ID NO 5
LENGTH: 7257

TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-102-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 6
US-09-567-969-5
Sequence 5, Application US/09567969
Patent No. 6355457
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/567,969
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-567-969-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 7
US-09-568-480-5
Sequence 5, Application US/09568480
Patent No. 6355458
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,480
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-480-5

Query Match 11.9%; Score 7; DB 4; Length 7257;

Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 8
US-09-568-486-5
Sequence 5, Application US/09568486
Patent No. 6355459
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,486
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-486-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||
Db 7250 SLARAK 7256

RESULT 9
US-09-568-472-5
Sequence 5, Application US/09568472
Patent No. 6358719
GENERAL INFORMATION:
APPLICANT: Schupp, Thomas
APPLICANT: Ligon, James
APPLICANT: Molnar, Istvan
APPLICANT: Zirkle, Ross
APPLICANT: Cyr, Devon
APPLICANT: Goerlach, Joern
TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES
FILE REFERENCE: 4-30582A
CURRENT APPLICATION NUMBER: US/09/568,472
CURRENT FILING DATE: 2000-05-10
PRIOR APPLICATION NUMBER: 09/335,409
PRIOR FILING DATE: 1999-06-17
NUMBER OF SEQ ID NOS: 30
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 5
LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum
US-09-568-472-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLARAK 11
|||||||

Db 7250 SLRACK 7256

RESULT 10

US-09-567-899-5
; Sequence 5, Application US/09567899

Patent No. 6383787
; GENERAL INFORMATION:

APPLICANT: Schnupp, Thomas

APPLICANT: Ligon, James

APPLICANT: Molnar, Istvan

APPLICANT: Zirkle, Ross

APPLICANT: Cyr, Devon

APPLICANT: Goerlach, Joern
; TITLE OF INVENTION: GENES FOR THE BIOSYNTHESIS OF EPOTHILONES

FILE REFERENCE: 4-30582A

CURRENT APPLICATION NUMBER: US/09/567,899
CURRENT FILING DATE: 2000-05-10

PRIOR FILING DATE: 1999-06-17

NUMBER OF SEQ ID NOS: 30
SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO 5

LENGTH: 7257
TYPE: PRT
ORGANISM: Sorangium cellulosum

US-09-567-899-5

Query Match 11.9%; Score 7; DB 4; Length 7257;
Best Local Similarity 100.0%; Pred. No. 95;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLRACK 11
|||||

Db 7250 SLRACK 7256

RESULT 11

US-09-082-358B-24
; Sequence 24, Application US/09082358B

Patent No. 6469153
; GENERAL INFORMATION:

APPLICANT: Goff, Stephen P.

APPLICANT: Li, Xingquiang

TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
FILE REFERENCE: 0575/54804

CURRENT APPLICATION NUMBER: US/09/082,358B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 24

LENGTH: 15

TYPE: PRT
ORGANISM: murine

US-09-082-358B-24

Query Match 10.2%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
|||||

Db 5 EKKKK 10

RESULT 12

US-09-082-358B-62
; Sequence 62, Application US/09082358B

Patent No. 6469153
; GENERAL INFORMATION:

APPLICANT: Goff, Stephen P.

APPLICANT: Li, Xingquiang

; TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
FILE REFERENCE: 0575/54804

CURRENT APPLICATION NUMBER: US/09/082,358B

CURRENT FILING DATE: 1998-05-20

NUMBER OF SEQ ID NOS: 106
SOFTWARE: PatentIn Ver. 2.1

SEQ ID NO 62

LENGTH: 15
TYPE: PRT
ORGANISM: murine

US-09-082-358B-62

Query Match 10.2%; Score 6; DB 4; Length 15;
Best Local Similarity 100.0%; Pred. No. 6.8;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
|||||

Db 10 EKKKK 15

RESULT 13

US-08-851-843A-201
; Sequence 201, Application US/08851843A

Patent No. 6093809
; GENERAL INFORMATION:

APPLICANT: Cech, Thomas R.

APPLICANT: Lingner, Joachim

APPLICANT: Nakamura, Toru

APPLICANT: Chapman, Karen B.

APPLICANT: Morin, Gregg B.

APPLICANT: Harley, Calvin

APPLICANT: Andrews, William H.
; TITLE OF INVENTION: No. 6093809e1 Telomerase

NUMBER OF SEQUENCES: 225

CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor

CITY: San Francisco

STATE: California

COUNTRY: United States of America

ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/851,843A

FILING DATE: 06-MAY-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017

FILING DATE: 25-APR-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419

FILING DATE: 18-APR-1997

CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643

FILING DATE: 01-OCT-1996

CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.

REGISTRATION NUMBER: 36/429

REFERENCE/DOCKET NUMBER: 015389-002930US

TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300

INFORMATION FOR SEQ ID NO: 201:

SEQUENCE CHARACTERISTICS:

LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-851-843A-201

Query Match 10.2%; Score 6; DB 3; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|11111|
Db 8 EKKKK 13

RESULT 14
US-08-974-549A-320
Sequence 320, Application US/08974549A
Patent No. 6166178

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: Human Telomerase Catalytic Subunit
NUMBER OF SEQUENCES: 727
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111-3834

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/974,549A
FILING DATE: 19-NOV-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/911,312
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/912,951
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/915,503
FILING DATE: 14-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17618
FILING DATE: 01-OCT-1997

PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US97/17885
FILING DATE: 01-OCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph Ted
REGISTRATION NUMBER: 36,429
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
FAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 320:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-974-549A-320

Query Match 10.2%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|11111|
Db 8 EKKKK 13

RESULT 15
US-08-854-050-201
Sequence 201, Application US/08854050
Patent No. 6261836

GENERAL INFORMATION:
APPLICANT: Cech, Thomas R.
APPLICANT: Lingner, Joachim
APPLICANT: Nakamura, Toru
APPLICANT: Chapman, Karen B.
APPLICANT: Morin, Gregg B.
APPLICANT: Harley, Calvin B.
APPLICANT: Andrews, William H.
TITLE OF INVENTION: No. 6261836el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/854,050
FILING DATE: 09-MAY-1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

CLASSIFICATION: 536
ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-854-050-201

Query Match 10.2%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
Db 8 EKKKK 13

RESULT 16
US-09-430-323-201
Sequence 201, Application US/09430323
Patent No. 6309867
GENERAL INFORMATION:
APPLICANT: Cecch, Thomas R.
Lingner, Joachim
Nakamura, Toru
Chapman, Karen B.
Mortin, Gregg B.
Harley, Calvin
Andrews, William H.

TITLE OF INVENTION: No. 6309867el Telomerase
NUMBER OF SEQUENCES: 225
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
CITY: San Francisco
STATE: California
COUNTRY: United States of America
ZIP: 94111

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/430,323
FILING DATE: 29-Oct-1999
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/854,050
FILING DATE: 09-MAY-1997
APPLICATION NUMBER: US 08/851,843
FILING DATE: 06-MAY-1997
APPLICATION NUMBER: US 08/846,017
FILING DATE: 25-APR-1997
APPLICATION NUMBER: US 08/844,419
FILING DATE: 18-APR-1997
APPLICATION NUMBER: US 08/724,643
FILING DATE: 01-OCT-1996

ATTORNEY/AGENT INFORMATION:
NAME: Apple, Randolph T.
REGISTRATION NUMBER: 36,429
REFERENCE/DOCKET NUMBER: 015389-00293005
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 576-0200

TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 201:
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
TOPOLOGY: linear
MOLECULE TYPE: peptide
SEQUENCE DESCRIPTION: SEQ ID NO: 201:
US-09-430-323-201

Query Match 10.2%; Score 6; DB 4; Length 16;
Best Local Similarity 100.0%; Pred. No. 7.2;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
|||||
Db 8 EKKKK 13

RESULT 17
US-09-177-249-189
Sequence 189, Application US/09177249
Patent No. 6229064
GENERAL INFORMATION:
APPLICANT: Fischer, Robert L.
APPLICANT: Ohad, Nir
APPLICANT: Kiyosue, Tomohiro
APPLICANT: Yadegarl, Ramlin
APPLICANT: Margossian, Linda
APPLICANT: Harada, John
APPLICANT: Goldberg, Robert B.
TITLE OF INVENTION: The Regents of the University of California
TITLE OF INVENTION: Nucleic Acids That Control Seed and Fruit
FILE REFERENCE: 023070-086120US
CURRENT APPLICATION NUMBER: US/09/177,249
CURRENT FILING DATE: 1998-10-22
EARLIER APPLICATION NUMBER: US 09/071,838
EARLIER FILING DATE: 1998-05-01
NUMBER OF SEQ ID NOS: 324
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 189
LENGTH: 29
TYPE: PRT
ORGANISM: Arabidopsis sp.
US-09-177-249-189

Query Match 10.2%; Score 6; DB 4; Length 29;
Best Local Similarity 100.0%; Pred. No. 12;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 TFGKK 53
|||||
Db 1 TFGKK 6

RESULT 18
US-09-227-357-479
Sequence 479, Application US/09227357
Patent No. 6342581
GENERAL INFORMATION:
APPLICANT: Fischer et al.
TITLE OF INVENTION: 123 Human Secreted Proteins
FILE REFERENCE: P2010P1
CURRENT APPLICATION NUMBER: US/09/227,357
CURRENT FILING DATE: 1999-01-08
EARLIER APPLICATION NUMBER: PCT/US98/13684
EARLIER FILING DATE: 1998-07-07
EARLIER APPLICATION NUMBER: 60/051,926
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,793
EARLIER FILING DATE: 1997-07-08

EARLIER APPLICATION NUMBER: 60/051,925
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,929
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,803
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,732
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,931
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,932
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,916
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,930
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,918
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,920
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,733
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/052,795
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,919
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/051,928
EARLIER FILING DATE: 1997-07-08
EARLIER APPLICATION NUMBER: 60/055,722
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,723
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,948
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,949
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,953
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,950
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,947
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,964
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/056,360
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,684
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,984
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/055,954
EARLIER FILING DATE: 1997-08-18
EARLIER APPLICATION NUMBER: 60/058,785
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,664
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,660
EARLIER FILING DATE: 1997-09-12
EARLIER APPLICATION NUMBER: 60/058,661
EARLIER FILING DATE: 1997-09-12
NUMBER OF SEQ ID NOS: 672
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 479
LENGTH: 51
TYPE: PRT
ORGANISM: Homo sapiens
US-09-227-357-479

Query Match 10.2%; Score 6; DB 4; Length 51;
Best Local Similarity 100.0%; Pred. No. 19;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 EKKKK 28

Db 35 EKKKK 40

RESULT 19

US-08-569-749-5

; Sequence 5, Application US/08569749

; Patent No. 6187557

; GENERAL INFORMATION:

; APPLICANT: Rothe, Mike

; APPLICANT: Goeddel, David V

; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/569,749

; FILING DATE:

; CLASSIFICATION: 514

; ATTORNEY/AGENT INFORMATION:

; NAME: Brezner, David J.

; REGISTRATION NUMBER: 24,774

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: (415)781-1989

; TELEFAX: (415)398-3249

; INFORMATION FOR SEQ ID NO: 5:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 55 amino acids

; TYPE: amino acid

; STRANDEDNESS: single

; TOPOLOGY: linear

; MOLECULE TYPE: protein

US-08-569-749-5

Query Match 10.2%; Score 6; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 5 SLRAG 10

Db 22 SLRAG 27

RESULT 20

US-08-569-749-6

; Sequence 6, Application US/08569749

; Patent No. 6187557

; GENERAL INFORMATION:

; APPLICANT: Rothe, Mike

; APPLICANT: Goeddel, David V

; TITLE OF INVENTION: INHIBITORS OF APOPTOSIS

; NUMBER OF SEQUENCES: 14

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: FLEHR, HOBBACH, TEST, ALBRITTON & HERBERT

; STREET: 4 Embarcadero Center, Suite 3400

; CITY: San Francisco

; STATE: California

; COUNTRY: USA

; ZIP: 94111

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/569,749
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-569-749-6

Query Match 10.2%; Score 6; DB 4; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 22 SLARAG 27

RESULT 21

PCT-US96-12860-5
Sequence 5, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-5

Query Match 10.2%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 22 SLARAG 27

RESULT 22

PCT-US96-12860-6
Sequence 6, Application PC/TUS9612860
GENERAL INFORMATION:
APPLICANT: TULARIK, INC.
TITLE OF INVENTION: INHIBITORS OF APOPTOSIS
NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
ADDRESSEE: FLEHR, HOHBACH, TEST, ALBRITTON & HERBERT
STREET: 4 Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94111
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US96/12860
FILING DATE: 06 AUG 1996
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: U.S. Serial Nos. 08/512,946 & 08/569,749
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Brezner, David J.
REGISTRATION NUMBER: 24,774
REFERENCE/DOCKET NUMBER: A-62464/DJB
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)781-1989
TELEFAX: (415)398-3249
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 55 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
PCT-US96-12860-6

Query Match 10.2%; Score 6; DB 5; Length 55;
Best Local Similarity 100.0%; Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 22 SLARAG 27

RESULT 23

US-09-082-358B-43
Sequence 43, Application US/09082358B
Patent No. 6469153
GENERAL INFORMATION:
APPLICANT: Goff, Stephen P.
TITLE OF INVENTION: EIP-1, EIP-3 GENES, ENVELOPE-INTERACTING PROTEINS,
FILE REFERENCE: 0575/54804
CURRENT APPLICATION NUMBER: US/09/082,358B
CURRENT FILING DATE: 1998-05-20
NUMBER OF SEQ ID NOS: 106

SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 43
; LENGTH: 57
; TYPE: PRT
; ORGANISM: murine
US-09-082-358B-43

Query Match 10.2%: Score 6; DB 4; Length 57;
Best Local Similarity 100.0%: Pred. No. 20;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKK 29
Db 51 KKKKK 56

RESULT 24
US-08-971-089-2
; Sequence 2, Application US/08971089
; Patent No. 6376174
; GENERAL INFORMATION:
; APPLICANT: Pulst, Stefan M.
; APPLICANT: Scoles, Daniel R.
; TITLE OF INVENTION: NUCLEIC ACID ENCODING
; TITLE OF INVENTION: SCHWANNOMIN-BINDING-PROTEINS AND PRODUCTS RELATED THERETO
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: CAMPBELL & FLORES, LLP
; STREET: 4370 La Jolla Village Drive, Suite 700
; CITY: San Diego
; STATE: California
; COUNTRY: United States
; ZIP: 92122
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/971,089
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 60/030,987
; FILING DATE: 15-NOV-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Ramos, Robert T.
; REGISTRATION NUMBER: 37,915
; REFERENCE/DOCKET NUMBER: P-CE 2862
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (619)535-9001
; TELEFAX: (619)535-8949
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 63 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-971-089-2

Query Match 10.2%: Score 6; DB 4; Length 63;
Best Local Similarity 100.0%: Pred. No. 22;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 23 EKKKK 28
Db 15 EKKKK 20

RESULT 25
US-08-511-485-18
; Sequence 18, Application US/08511485
; Patent No. 5919912

GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/511,485
; FILING DATE: 04-AUG-1995
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Clark, Paul T.
; REGISTRATION NUMBER: 30,162
; REFERENCE/DOCKET NUMBER: 07540/002001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 68 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: both
; MOLECULE TYPE: protein
US-08-511-485-18

Query Match 10.2%: Score 6; DB 2; Length 68;
Best Local Similarity 100.0%: Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 21 SLARAG 26

RESULT 26
US-08-511-485-19
; Sequence 19, Application US/08511485
; Patent No. 5919912
; GENERAL INFORMATION:
; APPLICANT: Korneluk, Robert G.
; APPLICANT: Mackenzie, Alexander E.
; APPLICANT: Baird, Stephen
; TITLE OF INVENTION: MAMMALIAN IAP GENE FAMILY, PRIMERS,
; TITLE OF INVENTION: PROBES, AND DETECTION METHODS
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/511,485
FILING DATE: 04-AUG-1995
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 07540/002001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ. ID NO: 19:
SEQUENCE CHARACTERISTICS:
LENGTH: 68 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: both
MOLECULE TYPE: protein
US-08-511-485-19

Query Match 10.2%; Score 6; DB 2; Length 68;
Best Local Similarity 100.0%; Pred. No. 23;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 5 SLARAG 10
Db 21 SLARAG 26

RESULT 27

US-09-091-725-51
Sequence 51, Application US/09091725
Patent No. 6329141
GENERAL INFORMATION:
APPLICANT:
TITLE OF INVENTION: Improved methods for transforming *Plasmodium*
NUMBER OF INVENTION: and recombinant DNA for use therein
NUMBER OF SEQUENCES: 51
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Morrison & Foerster LLP
STREET: 2000 Pennsylvania Avenue, N.W.
CITY: Washington
STATE: DC
COUNTRY: United States of America
ZIP: 20006-1888
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/091,725
FILING DATE: 23-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: EP 95203620.0
FILING DATE: 22-DEC-1995
APPLICATION NUMBER: EP 96200943.7
FILING DATE: 11-APR-1996
ATTORNEY/AGENT INFORMATION:
NAME: E. Victor Donahue
REGISTRATION NUMBER: 35,492
INFORMATION FOR SEQ. ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 141 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-091-725-51

Query Match 10.2%; Score 6; DB 4; Length 141;
Best Local Similarity 100.0%; Pred. No. 43;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 48 TFGKKK 53
Db 7 TFGKKK 12

RESULT 28

US-08-871-732A-1
Sequence 1, Application US/08871732A
Patent No. 6140074
GENERAL INFORMATION:
APPLICANT: O'BRIEN, TIMOTHY J.
TITLE OF INVENTION: NOVEL SH3 PROTEIN, GENE, CHIMERIC
TITLE OF INVENTION: CELLS, VECTORS AND EXPRESSION METHOD FOR PRODUCING THE NOVE
TITLE OF INVENTION: PROTEIN, ANTIBODIES AND USES
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESSES:
ADDRESSEE: MARTIN L. MCGREGOR
STREET: 5380 WEST 34TH STREET, #345
CITY: HOUSTON
STATE: TEXAS
COUNTRY: UNITED STATES OF AMERICA
ZIP: 77092
COMPUTER READABLE FORM:
MEDIUM TYPE: DISKETTE 3.5 INCH 1.44 MB STORAGE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: MS-DOS
SOFTWARE: WORDPERFECT 6.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/871,732A
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: MCGREGOR, MARTIN L.
REGISTRATION NUMBER: 29,329
REFERENCE/DOCKET NUMBER: 1-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: 713-682-1213
TELEFAX: 713-682-5807
TELEX: NONE
INFORMATION FOR SEQ. ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 154 AMINO ACIDS
TYPE: AMINO ACID
STRANDEDNESS: SINGLE
TOPOLOGY: LINEAR
MOLECULE TYPE: PROTEIN
US-08-871-732A-1

Query Match 10.2%; Score 6; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 46;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 24 KKKKKT 29
Db 66 KKKKKT 71

RESULT 29

US-09-346-510B-1
Sequence 1, Application US/09346510B
Patent No. 6281014
GENERAL INFORMATION:
APPLICANT: O'Brien, Timothy J.
TITLE OF INVENTION: SH3-Containing protein, DNA and uses thereof
FILE REFERENCE: D6221CIP
CURRENT APPLICATION NUMBER: US/09/346,510B
CURRENT FILING DATE: 1999-07-01
PRIOR APPLICATION NUMBER: 08/871,732
PRIOR FILING DATE: 1997-06-09

NUMBER OF SEQ ID NOS: 32
SEQ ID NO 1
LENGTH: 154
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: amino acid sequence of TADG5 protein
US-09-346-510B-1

Query Match
Best Local Similarity 10.2%; Score 6; DB 4; Length 154;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKKT 29
Db 66 KKKKKT 71

RESULT 30
US-08-533-669A-4
Sequence 4, Application US/08533669A
Patent No. 5834592
GENERAL INFORMATION:
APPLICANT: Corixa Corporation
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE
TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF LEISHMANIASIS
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/533,669A
FILING DATE: 22-SEP-1995
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-533-669A-4

Query Match
Best Local Similarity 10.2%; Score 6; DB 2; Length 175;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AKRRMQ 37
Db 160 AKRRMQ 165

RESULT 31
US-09-183-861-4
Sequence 4, Application US/09183861
Patent No. 6365165
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.

APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/183,861
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 09/022,765
FILING DATE: 12-FEB-1998
ATTORNEY/AGENT INFORMATION:
NAME: MAKI, David J.
REGISTRATION NUMBER: 31,392
REFERENCE/DOCKET NUMBER: 210121.420C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: (206) 622-4900
TELEFAX: (206) 682-6031
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 175 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-09-183-861-4

Query Match
Best Local Similarity 10.2%; Score 6; DB 4; Length 175;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 32 AKRRMQ 37
Db 160 AKRRMQ 165

RESULT 32
US-09-022-765-4
Sequence 4, Application US/09022765
Patent No. 6375955
GENERAL INFORMATION:
APPLICANT: Reed, Steven G.
APPLICANT: Campos-Neto, Antonio
APPLICANT: Webb, John R.
APPLICANT: Dillon, Davin C.
APPLICANT: Skeiky, Yasir A.W.
TITLE OF INVENTION: LEISHMANIA ANTIGENS FOR USE IN THE THERAPY AND
NUMBER OF SEQUENCES: 87
CORRESPONDENCE ADDRESS:
ADDRESSEE: SEED and BERRY LLP
STREET: 6300 Columbia Center, 701 Fifth Avenue
CITY: Seattle
STATE: Washington
COUNTRY: USA
ZIP: 98104-7092
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30

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; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,765
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: MAKI, David J.
; REGISTRATION NUMBER: 31,392
; REFERENCE/DOCKET NUMBER: 210121.420C3
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (206) 622-4900
; TELEFAX: (206) 682-6031
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 175 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-022-765-4

Query Match
Best Local Similarity 10.2%; Score 6; DB 4; Length 175;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 32 AKRRMQ 37
Db 160 AKRRMQ 165

RESULT 33
US-08-468-347-24
; Sequence 24, Application US/08468347
; Patent No. 5783421
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/468,347
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
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; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..197
; US-08-468-347-24

Query Match
Best Local Similarity 10.2%; Score 6; DB 1; Length 197;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 KKKKKT 29
Db 191 KKKKKT 196

RESULT 34
US-08-467-389-24
; Sequence 24, Application US/08467389
; Patent No. 5824641
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/467,389
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPW/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..197
; US-08-467-389-24

Query Match
Best Local Similarity 10.2%; Score 6; DB 2; Length 197;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 24 KKKKKT 29
Db 191 KKKKKT 196
```

RESULT 35
US-08-779-379-24
; Sequence 24, Application US/08779379
; Patent No. 5858970
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; NUMBER OF SEQUENCES: 25
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Cooper & Dunham
; STREET: 30 Rockefeller Plaza
; CITY: New York
; STATE: New York
; COUNTRY: USA
; ZIP: 10112
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,379
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/225,442
; FILING DATE: 08-APR-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: White, John P.
; REGISTRATION NUMBER: 28,678
; REFERENCE/DOCKET NUMBER: 0317/43020-A/JPM/EAB
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 212-977-9550
; TELEFAX: 212-664-0525
; INFORMATION FOR SEQ ID NO: 24:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 197 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Protein
; LOCATION: 1..197
US-08-779-379-24
Query Match 10.2%; Score 6; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
| | | | |
Db 191 KKKKT 196

RESULT 36
US-08-469-219-24
; Sequence 24, Application US/08469219
; Patent No. 5863534
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa
; TITLE OF INVENTION: INHIBITORY ACTIVITY

NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham
STREET: 30 Rockefeller Plaza
CITY: New York
STATE: New York
ZIP: 10112
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,219
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/225,442
FILING DATE: 08-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0317/43020-A/JPM/EAB
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-977-9550
TELEFAX: 212-664-0525
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 197 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
FEATURE:
NAME/KEY: Protein
LOCATION: 1..197
US-08-469-219-24
Query Match 10.2%; Score 6; DB 2; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
| | | | |
Db 191 KKKKT 196

RESULT 37
US-09-228-152-24
; Sequence 24, Application US/09228152
; Patent No. 6211341
; GENERAL INFORMATION:
; APPLICANT: Zeelon, Elisha P.
; APPLICANT: Werber, Moshe M.
; APPLICANT: Levanon, Avigdor
; TITLE OF INVENTION: NOVEL POLYPEPTIDE HAVING FACTOR Xa INHIBITORY ACTIVITY
; FILE REFERENCE: 43020aYa
; CURRENT APPLICATION NUMBER: US/09/228,152
; CURRENT FILING DATE: 1999-01-11
; SOFTWARE: Patentin Ver. 2.0
; NUMBER OF SEQ ID NOS: 25
; SEQ ID NO 24
; LENGTH: 197
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Deduced amino
; OTHER INFORMATION: acid sequence of clone pSP65-Xa1-13.
US-09-228-152-24

Query Match 10.2%; Score 6; DB 4; Length 197;
Best Local Similarity 100.0%; Pred. No. 56;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
111111
DB 191 KKKKT 196

RESULT 38

US-08-903-801-3
; Sequence 3, Application US/08903801
; Patent No. 5932712
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer
; APPLICANT: Corley, Neil C.
; TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/903,801
; FILING DATE: Herewith
; CLASSIFICATION: 536
; PRIOR APPLICATION NUMBER:
; ATTORNEY/AGENT INFORMATION:
; FILING DATE:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0354 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1514949
; US-08-903-801-3

Query Match 10.2%; Score 6; DB 2; Length 234;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
111111
DB 217 KKKKT 222

RESULT 39

US-09-295-055-3
; Sequence 3, Application US/09295055
; Patent No. 6232440
; GENERAL INFORMATION:
; APPLICANT: Hillman, Jennifer
; APPLICANT: Corley, Neil C.

APPLICANT: Shah, Purvi
; TITLE OF INVENTION: NEW ANEXIN BINDING PROTEIN
; NUMBER OF SEQUENCES: 3
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Incyte Pharmaceuticals, Inc.
; STREET: 3174 Porter Drive
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FASTSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/295,055
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/903,801
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Billings, Lucy J.
; REGISTRATION NUMBER: 36,749
; REFERENCE/DOCKET NUMBER: PF-0354 US
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-855-0555
; TELEFAX: 415-845-4166
; TELEX:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 234 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GenBank
; CLONE: 1514949
; US-09-295-055-3

Query Match 10.2%; Score 6; DB 4; Length 234;
Best Local Similarity 100.0%; Pred. No. 64;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 24 KKKKT 29
111111
DB 217 KKKKT 222

RESULT 40

US-09-149-476-568
; Sequence 568, Application US/09149476
; Patent No. 6420526
; GENERAL INFORMATION:
; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 166 Human secreted proteins
; FILE REFERENCE: P2002P1
; CURRENT APPLICATION NUMBER: US/09/149,476
; EARLIER FILING DATE: 1998-09-08
; EARLIER APPLICATION NUMBER: PCT/US98/04493
; EARLIER FILING DATE: 1998-03-06
; EARLIER APPLICATION NUMBER: 60/040,162
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,333
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/038,621
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,626
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,334
; EARLIER FILING DATE: 1997-03-07
; EARLIER APPLICATION NUMBER: 60/040,336

EARLIER APPLICATION NUMBER:	60/056,886
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,877
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,889
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,893
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,630
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,878
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,662
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,872
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,903
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,888
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,879
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,880
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,894
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,911
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,636
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,874
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,910
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,864
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/056,631
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/057,761
EARLIER FILING DATE:	1997-08-22
EARLIER APPLICATION NUMBER:	60/047,595
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,599
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,588
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,585
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,586
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,590
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,594
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,589
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,593
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/047,614
EARLIER FILING DATE:	1997-05-23
EARLIER APPLICATION NUMBER:	60/043,578
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/043,576
EARLIER FILING DATE:	1997-04-11
EARLIER APPLICATION NUMBER:	60/047,501

; EARLIER FILING DATE: 1997-05-23
; EARLIER APPLICATION NUMBER: 60/043,670
; EARLIER FILING DATE: 1997-04-11
; EARLIER APPLICATION NUMBER: 60/056,632
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,664
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,876
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,881
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,909
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,875
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,862
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,887
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/056,908
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/048,964
; EARLIER FILING DATE: 1997-06-06
; EARLIER APPLICATION NUMBER: 60/057,650
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/056,884
; EARLIER FILING DATE: 1997-08-22
; EARLIER APPLICATION NUMBER: 60/057,669
; EARLIER FILING DATE: 1997-09-05
; EARLIER APPLICATION NUMBER: 60/049,610
; EARLIER FILING DATE: 1997-06-13
; EARLIER APPLICATION NUMBER: 60/061,060
; EARLIER FILING DATE: 1997-10-02

Query Match 10.2%; Score 6; DB 4; Length 251;
Best Local Similarity 100.0%; Pred. No. 68;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 23 EKKKK 28
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DB 245 EKKKK 250

RESULT 41
US-09-347-803-20
; Sequence 20, Application US/09347803
; Patent No. 6274379
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hiltz, Bill
; APPLICANT: Kinney, Tony
; APPLICANT: Orozco, Buddy
; TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
; FILE REFERENCE: BB-1176
; CURRENT APPLICATION NUMBER: US/09/347,803
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,952
; EARLIER FILING DATE: July 15, 1998
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 20
; LENGTH: 316
; TYPE: PRT
; ORGANISM: Glycine max
US-09-347-803-20

Query Match 10.2%; Score 6; DB 4; Length 316;
Best Local Similarity 100.0%; Pred. No. 82;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHGSIA 7
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DB 134 VHGSIA 139

RESULT 42
US-09-615-192A-389
; Sequence 389, Application US/09615192A
; Patent No. 6410718
; GENERAL INFORMATION:
; APPLICANT: Bloksberg, Leonard N.
; APPLICANT: Havukkala, Ilkka
; TITLE OF INVENTION: Materials and Methods for the
; FILE REFERENCE: 11000.1003c4U
; CURRENT APPLICATION NUMBER: US/09/615,192A
; CURRENT FILING DATE: 2000-07-12
; PRIOR APPLICATION NUMBER: US 08/975,316
; PRIOR FILING DATE: 1997-11-21
; PRIOR APPLICATION NUMBER: US 08/713,000
; PRIOR FILING DATE: 1996-09-11
; PRIOR APPLICATION NUMBER: US 09/169,789
; PRIOR FILING DATE: 1998-10-09
; NUMBER OF SEQ ID NOS: 405
; SOFTWARE: PastSeq for Windows Version 3.0
; SEQ ID NO 389
; LENGTH: 318
; TYPE: PRT
; ORGANISM: Pinus radiata
US-09-615-192A-389

Query Match 10.2%; Score 6; DB 4; Length 318;
Best Local Similarity 100.0%; Pred. No. 83;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 54 GPNANS 59
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DB 92 GPNANS 97

RESULT 43
US-09-347-803-16
; Sequence 16, Application US/09347803
; Patent No. 6274379
; GENERAL INFORMATION:
; APPLICANT: Famodu, Layo O.
; APPLICANT: Hiltz, Bill
; APPLICANT: Kinney, Tony
; APPLICANT: Orozco, Buddy
; TITLE OF INVENTION: Plant Sorbitol Biosynthetic Enzymes
; FILE REFERENCE: BB-1176
; CURRENT APPLICATION NUMBER: US/09/347,803
; CURRENT FILING DATE: 1999-07-02
; EARLIER APPLICATION NUMBER: 60/092,952
; EARLIER FILING DATE: July 15, 1998
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Microsoft Office 97
; SEQ ID NO 16
; LENGTH: 341
; TYPE: PRT
; ORGANISM: Zea mays
US-09-347-803-16

Query Match 10.2%; Score 6; DB 4; Length 341;
Best Local Similarity 100.0%; Pred. No. 88;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 2 VHGSIA 7
|||||
DB 126 VHGSIA 131

RESULT 44
US-08-729-214-27
; Sequence 27, Application US/08729214
; Patent No. 5817502

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;
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight Steven
; APPLICANT: Ryals, John Andrew
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; TITLE OF INVENTION: Genes for the synthesis of
; TITLE OF INVENTION: antipathogenic substances
; NUMBER OF SEQUENCES: 27
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Ciba-Geigy Corporation
; STREET: 520 White Plains Road
; CITY: Tarrytown
; STATE: NY
; COUNTRY: USA
; ZIP: 10591
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/729,214
; FILING DATE: TBA
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC 1506/CIP5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-08-729-214-27

Query Match          10.2%; Score 6; DB 2; Length 370;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 SLARAG 10
        |||||
Db      214 SLARAG 219

RESULT 45
US-09-028-934-27
; Sequence 27, Application US/09028934
; Patent No. 6117670
; GENERAL INFORMATION:
; APPLICANT: Ligon, James M.
; APPLICANT: Hill, Dwight S.
; APPLICANT: Lam, Steven T.
; APPLICANT: Hammer, Phillip E.
; APPLICANT: van Pee, Karl-Heinz
; APPLICANT: Kirner, Sabine
; APPLICANT: Young, Thomas R.
; TITLE OF INVENTION: Pyroglutinin Biosynthesis Genes and Uses
; TITLE OF INVENTION: Thereof
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: No. 6117670artis Corporation
; STREET: 3054 Cornwallis Road
; CITY: Research Triangle Park
; STATE: NC
; COUNTRY: USA
; ZIP: 27709
; COMPUTER READABLE FORM:
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; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
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; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/729,214
; FILING DATE: 09-OCT-1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/258,261
; FILING DATE: 08-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Meigs, J. Timothy
; REGISTRATION NUMBER: 38,241
; REFERENCE/DOCKET NUMBER: CGC1506/CIP7
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 919-541-8587
; TELEFAX: 919-541-8689
; INFORMATION FOR SEQ ID NO: 27:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 370 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; US-09-028-934-27

Query Match          10.2%; Score 6; DB 3; Length 370;
Best Local Similarity 100.0%; Pred. No. 94;
Matches 6; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      5 SLARAG 10
        |||||
Db      214 SLARAG 219
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Job time : 17 secs

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GenCore version 5.1.3
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: February 6, 2003, 21:09:24 : Search time 35 Seconds
(without alignments)
224.622 Million cell updates/sec

Title: US-09-424-815E-1

Perfect score: 59
Sequence: 1 KKHGSLARAGKVGCRPKVA.....RRVVNVPTFGKKKGNNANS 59

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 908470 seqs, 133250620 residues

Word size : 0

Total number of hits satisfying chosen parameters: 908470

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result NO.	Score	Query Match	Length	DB ID	Description
1	59	100.0	59	15	AAK48204
2	59	100.0	59	20	AAW5381
3	59	100.0	66	23	ABP42408
4	59	100.0	170	21	AAW43549
5	41	69.5	41	17	AAW03681
6	39	66.1	108	22	ABG27228
7	39	66.1	108	22	ABG27519
8	37	62.7	40	22	AAO08731
9	37	62.7	157	22	AAW5965
10	32	54.2	130	21	AAW01569

11	32	54.2	312	22	AAU30872	Novel human secret
12	31	52.5	61	22	ABG27230	Novel human diagno
13	31	52.5	90	22	ABG27520	Novel human diagno
14	28	47.5	118	22	ABG29449	Peptide #2100 enco
15	28	47.5	118	22	ABG34625	Peptide #2131 enco
16	28	47.5	118	22	ABG20035	Protein #2034 enco
17	28	47.5	118	22	AAW55415	Human brain expres
18	28	47.5	118	22	AAW67811	Human bone marrow
19	28	47.5	118	22	AAW15620	Peptide #2054 enco
20	28	47.5	118	22	AAW28118	Peptide #2155 enco
21	28	47.5	118	22	AAW03364	Peptide #2046 enco
22	28	47.5	118	23	ABG37354	Human peptide enco
23	24	40.7	35	22	AAO07113	Human polypeptide
24	22	37.3	62	21	AAW04311	Arabidopsis thalia
25	22	37.3	62	21	AAW15348	Arabidopsis thalia
26	22	37.3	62	21	AAW22753	Arabidopsis thalia
27	22	37.3	62	21	AAW32888	Zea mays protein f
28	22	37.3	62	21	AAW34119	Zea mays protein f
29	22	37.3	62	21	AAW38861	Arabidopsis thalia
30	22	37.3	62	21	AAW39476	Arabidopsis thalia
31	22	37.3	62	21	AAW40704	Zea mays protein f
32	22	37.3	62	21	AAW40788	Zea mays protein f
33	22	37.3	62	21	AAW44883	Zea mays protein f
34	22	37.3	62	21	AAW48690	Arabidopsis thalia
35	22	37.3	68	21	AAW31871	Arabidopsis thalia
36	22	37.3	82	21	AAW40703	Zea mays protein f
37	22	37.3	84	21	AAW44882	Zea mays protein f
38	22	37.3	83	21	AAW32887	Zea mays protein f
39	22	37.3	93	21	AAW34118	Zea mays protein f
40	22	37.3	110	21	AAW32886	Zea mays protein f
41	22	37.3	130	21	AAW36788	Zea mays protein f
42	21	35.6	230	23	ABG34133	Human sebh protel
43	21	35.6	459	23	ABG34132	Human sebh protel
44	20	33.9	65	21	AAW20231	Arabidopsis thalia
45	19	32.2	229	22	AAU31057	Novel human secret

ALIGNMENTS

RESULT 1
AAK48204
ID AAK48204 standard; protein: 59 AA.
XX
AC AAK48204;
XX
DT 12-JUL-1994 (first entry)
XX
DE Heparin-binding protein.
XX
KW Cell growth agent; wound; bone disease; treatment; treating; agent.
XX
OS Rattus norvegicus.
XX
PN JF05339287-A.
XX
PD 21-DEC-1993.
XX
PE 05-JUN-1992; 92JP-0145125.
XX
PR 05-JUN-1992; 92JP-0145125.
XX
PA (FARH) HOECHST JAPAN LTD.
XX
DR WPI; 1994-031824/04.
XX
PT New heparin-binding protein - used as a cell growth agent for
XX treatment of wounds and bone disease
XX
PS Claim 1; Page 3; App; Japanese.
XX
CC The sequence is that of a heparin binding-protein which is useful as
a cell growth agent and in the treatment of wounds and bone disease.

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XX  Sequence      59 AA;
SQ
Query Match      100.0%; Score 59: DB 15: Length 59:
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db  1 KVHGSILARAGKVGQTPPKVAKOEKKKKKTGRARRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 2
AAW95381
ID  AAW95381 standard; peptide; 59 AA.
XX
AC  AAW95381:
XX
DT  17-MAR-1999 (first entry)
XX
DE  Antimicrobial peptide fragment from ubiQUiCIDiNE.
XX
KW  ubiQUiCIDiNE; treatment; diagnosis; prophylaxis; infection; microbial;
KW  pathogenic; Gram-positive bacteria; antimicrobial; Staphylococcus aureus;
KW  listeria monocytogenes; Gram-negative; Klebsiella pneumoniae; E. coli;
KW  enterococcus; Salmonella typhimurium; Mycobacterium avium; M. fortuitum;
KW  fungus; Candida albicans; Cryptococcus neoformans; Aspergillus fumigatus;
KW  virus; parasite; Trypanosoma cruzi; Toxoplasma gondii.
XX
OS  Synthetic.
OS  Mus sp.
XX
PN  WO9854314-A1.
XX
PD  03-DEC-1998.
XX
PE  29-MAY-1998: 98WO-NL00311.
XX
PR  29-MAY-1997: 97NL-1006164.
XX
PA  (UYLE-) RICKSUNIV LEIDEN.
XX
PI  Feltma RIJ, Hienstra PS, Nibbering PH, Pauwels EKJ;
PI  Van Den Barselaar MT;
XX
DR  WPI: 1999-070214/06.
XX
PT  New antimicrobial peptides derived from ubiQUiCIDiNE - useful for
PT  the prophylaxis, diagnosis and treatment of infections in humans and
PT  animals
XX
XX  Claim 2: Page 23; 48pp; English.
XX
CC  Sequences AAW95381-389 represent antimicrobial peptide fragments derived
CC  from ubiQUiCIDiNE. UbiQUiCIDiNE or optionally modified peptide fragments
CC  of ubiQUiCIDiNE, may be used for the treatment, diagnosis, or
CC  prophylaxis of infections in humans and animals. In particular the
CC  products and methods are directed against microbial infections caused by
CC  pathogenic Gram-positive Staphylococcus aureus, including antibiotic
CC  resistant strains; Listeria monocytogenes; and Gram-negative antibiotic
CC  resistant Klebsiella pneumoniae, E. coli, enterococci, and Salmonella
CC  typhimurium bacteria; micro-organisms difficult to treat such as
CC  Mycobacterium avium and M. fortuitum, fungi such as Candida albicans,
CC  Cryptococcus neoformans, and Aspergillus fumigatus, viruses, in
CC  particular enveloped viruses, and parasites such as Trypanosoma cruzi and
CC  Toxoplasma gondii.
XX
SQ  Sequence      59 AA;
Query Match      100.0%; Score 59: DB 20: Length 59:
Best Local Similarity 100.0%; Pred. No. 1.9e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

QY  1 KVHGSILARAGKVGQTPPKVAKOEKKKKKTGRARRMQYNRRFVNVVPTFGKKKGPNANS 59
Db  1 KVHGSILARAGKVGQTPPKVAKOEKKKKKTGRARRMQYNRRFVNVVPTFGKKKGPNANS 59

RESULT 3
ABP42408
ID  ABP42408 standard; Protein; 66 AA.
XX
AC  ABP42408:
XX
DT  22-AUG-2002 (first entry)
XX
DE  Human ovarian antigen HOCM79, SEQ ID NO:3540.
XX
KW  Human: ovarian antigen; ovary; ovarian; breast; cancer; tumour;
KW  ovarian cancer; breast cancer; tumour; reproductive system disorder;
KW  infertility; pregnancy disorder; anovulation; polycystic ovary syndrome;
KW  PCOS; ovarian cyst; dysmenorrhoea; endocrine disorder; infection;
KW  inflammatory condition; immune disorder; blood disorder;
KW  cardiovascular disorder; respiratory disorder; neurological disorder;
KW  gastrointestinal disorder; urinary system disorder; drug screening;
KW  gene therapy; chromosome mapping; forensic analysis;
KW  antibody preparation; cytostatic; immunomodulatory; neuroprotective;
KW  antiinflammatory; gynaecological; reproductive.
XX
OS  Homo sapiens.
XX
PN  WO200200677-A1.
XX
PD  03-JAN-2002.
XX
PE  07-JUN-2001: 2001WO-US18569.
XX
PR  07-JUN-2000: 2000US-209467P.
XX
PA  (HUMA-) HUMAN GENOME SCI INC.
XX
PI  Birse CE, Rosen CA;
XX
DR  WPI: 2002-147878/19.
XX
DR  N-PSDB: AB055485.
XX
PT  Isolated nucleic acid molecules encoding novel ovarian polypeptides,
PT  useful in the prevention, treatment and diagnosis of cancer (e.g.
PT  ovarian cancer), immune disorders, cardiovascular disorders and
PT  neurological diseases -
XX
XX  Claim 11: SEQ ID NO 3540; 2922pp; English.
XX
CC  The invention relates to 2175 novel human ovarian antigens (ABP41054-
CC  ABP43228) and to cDNAs encoding them (AB054131-AB056305), and also
CC  encompasses polypeptides 908 identical and polynucleotides 958 identical
CC  to the sequences of the invention. The invention additionally relates to
CC  recombinant vectors and host cells comprising human ovarian antigen
CC  polynucleotides, antibodies against human ovarian antigens, and the use
CC  of ovarian antigen polynucleotides and polypeptides in diagnosing,
CC  treating, prophosing or preventing various ovary and/or breast-related
CC  disorders. Such conditions include ovarian cancer and breast cancer, and
CC  metastatic tumours of ovarian or breast origin, reproductive system
CC  disorders (e.g., infertility, disorders of pregnancy, anovulation,
CC  polycystic ovary syndrome, ovarian cysts, and dysmenorrhoea), endocrine
CC  disorders, infections (e.g., chlamydia, HIV, toxoplasmosis, and toxic
CC  shock syndrome), inflammatory conditions (e.g., mastitis, oophoritis and
CC  vaginitis), immune disorders (e.g., congenital and acquired
CC  immunodeficiencies, autoimmune oophoritis, systemic lupus erythematosus),
CC  blood-related disorders (e.g., anaemia), cardiovascular disorders,
CC  respiratory disorders, neurological disorders, gastrointestinal disorders
CC  and urinary system disorders. Ovarian antigen polypeptides and
CC  polynucleotides may also be used in screening for compounds which
CC  modulate ovarian antigen expression or activity. The polynucleotides may
CC  further be used for gene therapy, chromosome mapping, in the
CC  identification of individuals and in forensic analysis, and the

```

CC polypeptides may be used as food additives or to prepare antibodies
CC useful in disease diagnosis, drug targeting and phenotyping. The present
CC sequence represents a human ovarian antigen of the invention. The present
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at http://wipo.int/pub/publ/published_pcl_sequences.

XX
SQ Sequence 66 AA;

Query Match 100.0%; Score 59; DB 23; Length 66;
Best Local Similarity 100.0%; Pred. No. 2.1e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSILARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNNNS 59
DB 8 KVHGSILARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNNNS 66

RESULT 4
AAB43549

ID AAB43549 standard; Protein; 170 AA.

XX
AC AAB43549;

XX
DT 08-FEB-2001 (first entry)

XX
DE Human cancer associated protein sequence SEQ ID NO:994.

XX Human: cancer associated gene; cancer antigen; detection; cancer;
KW diagnosis; cytostatic; proliferative; vulnerability; immunomodulator;
KW antidiabetic; antiallergic; antineumatic; antiarthritic; antiviral;
KW antinflammatory; antithyroid; antiallergic; antibacterial; cardiant;
KW dermatological; neuroprotective; thrombolytic; coagulant; nocitropic;
KW vasotropic; antipsoriatic; antiangiogenic; gene therapy; inflammation;
KW immune disorder; haematopoietic cell disorder; autoimmune disorder;
KW allergic reaction; graft versus host disease; organ rejection;
KW haemostatic; thrombolytic; cardiovascular disorder; infection;
KW neurological disease; drug screening.

XX
OS Homo sapiens.

XX
PN WO200055350-A1.

XX
PD 21-SEP-2000.

XX
PF 08-MAR-2000; 2000WO-US05882.

XX
PR 12-MAR-1999; 99US-0124270.

XX
PA (HUMA-) HUMAN GENOME SCI INC.

XX
PI Rosen CA, Ruben SM;

XX
DR WPI: 2000-587533/55.

XX
PT N-PSDB; AAC77758.

XX
PT Novel isolated nucleic acids comprising sequences encoding peptides
XX useful for treating or diagnosing e.g. cancer -

XX
PS Claim 11; Page 1568-1569; 2352pp; English.

XX
CC AAC77607 to AAC78448 encode the human cancer associated proteins given
CC in AAB43398 to AAB44239. The proteins can have activities based on the
CC tissues and cells the genes are expressed in. Example of activities
CC include: cytostatic; proliferative; vulnerability; immunomodulator;
CC antidiabetic; antiallergic; antineumatic; antiarthritic; antiviral;
CC antinflammatory; antithyroid; antiallergic; antibacterial; antiviral;
CC dermatological; neuroprotective; cardiant; thrombolytic; coagulant;
CC nocitropic; vasotropic; antipsoriatic and antiangiogenic. The
CC polynucleotides and polypeptides can be used for preventing, treating or
CC ameliorating medical conditions and diagnosing pathological conditions.
CC Polynucleotides, polypeptides, antibodies, agonists and antagonists from
CC the present invention may be used to treat immune disorders by activating

CC or inhibiting the proliferation, differentiation or mobilisation of
CC immune cells, to treat disorders of haematopoietic cells, autoimmune
CC disorders, allergic reactions, graft versus host disease and organ
CC rejection, modulate haemostatic or thrombolytic activity, modulate
CC inflammation, cancers, cardiovascular disorders, neurological disease and
CC bacterial or viral infections. The peptides, nucleotides, antibodies,
CC agonists and antagonists may be also be used in drug screens. AAC78449 to
CC AAC78457 and AAB44240 represent sequences used in the exemplification of
CC the present invention.

XX
SQ Sequence 170 AA;

Query Match 100.0%; Score 59; DB 21; Length 170;
Best Local Similarity 100.0%; Pred. No. 4.7e-54;
Matches 59; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSILARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNNNS 59
DB 112 KVHGSILARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRRFVNVVPTFGKKKGPNNNS 170

RESULT 5
AAW03681

ID AAW03681 standard; peptide; 41 AA.

XX
AC AAW03681;

XX
DT 31-DEC-1996 (first entry)

XX
DE Long term potentiation inducing peptide.

XX Long term potentiation inducing peptide; mouse; brain; senile dementia;
KW cerebrovascular; Alzheimer's disease.

XX
OS Mus musculus.

XX
PN JP08176193-A.

XX
PD 09-JUL-1996.

XX
PF 23-DEC-1994; 94JP-0336143.

XX
PR 23-DEC-1994; 94JP-0336143.

XX
PA (SOSE-) SOSEI KK.

XX
DR WPI: 1996-368226/37.

XX
PT A long-term potentiation inducing peptide - useful for the diagnosis
XX and treatment of senile dementia

XX
PS Claim 1; Page 6; 7pp; Japanese.

XX
CC This is the sequence of a long term potentiation inducing peptide
CC isolated from mice brains by centrifugation, extraction, dialysis
CC reverse phase HPLC and gel filtration chromatography (Sephadex C-25).
CC The peptide is useful for diagnosis and treatment of senile dementia
CC e.g. cerebrovascular or Alzheimer's dementias.

XX
SQ Sequence 41 AA;

Query Match 69.5%; Score 41; DB 17; Length 41;
Best Local Similarity 100.0%; Pred. No. 1.1e-35;
Matches 41; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSILARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRR 41
DB 1 KVHGSILARAGKVRGQTPKVAKEKKKKKTGRAKRRMQYNRR 41

RESULT 6
ABG27228
ID ABG27228 standard; Protein; 108 AA.

```
XX AC ABG27228;
XX XX
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #27219.
XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX KM food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS91415.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 57587; 103pp; English.
XX XX
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 108 AA:
XX
XX Query Match 66.1%; Score 39; DB 22; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-33;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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```
OY 20 AKOEKKKKKTGAKRRMOYNRRFVNVPFGKKKGPNN 58
DB 69 AKOEKKKKKTGAKRRMOYNRRFVNVPFGKKKGPNN 107
```

```
RESULT 7
ABG27519
ID ABG27519 standard; Protein; 108 AA.
XX
XX AC ABG27519;
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XX XX
XX DT 18-FEB-2002 (first entry)
XX DE Novel human diagnostic protein #27510.
XX KW Human: chromosome mapping; gene mapping; gene therapy; forensic;
XX KM food supplement; medical imaging; diagnostic; genetic disorder.
XX OS Homo sapiens.
XX PN WO200175067-A2.
XX PD 11-OCT-2001.
XX PF 30-MAR-2001; 2001WO-US08631.
XX PR 31-MAR-2000; 2000US-0540217.
XX PR 23-AUG-2000; 2000US-0649167.
XX PA (HYSE-) HYSEQ INC.
XX PI Drmanac RT, Liu C, Tang YT;
XX DR WPI: 2001-639362/73.
XX DR N-PSDB; AAS91706.
XX PT New isolated polynucleotide and encoded polypeptides, useful in
XX PT diagnostics, forensics, gene mapping, identification of mutations
XX PT responsible for genetic disorders or other traits and to assess
XX PT biodiversity.
XX PS Claim 20; SEQ ID NO 57878; 103pp; English.
XX XX
XX CC The invention relates to isolated polynucleotide (I) and
XX CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
XX CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
XX CC and gene mapping, and in recombinant production of (II). The
XX CC polynucleotides are also used in diagnostics as expressed sequence tags
XX CC for identifying expressed genes. (I) is useful in gene therapy techniques
XX CC to restore normal activity of (II) or to treat disease states involving
XX CC (II). (II) is useful for generating antibodies against it, detecting or
XX CC quantitating a polypeptide in tissue, as molecular weight markers and as
XX CC a food supplement. (II) and its binding partners are useful in medical
XX CC imaging of sites expressing (II). (I) and (II) are useful for treating
XX CC disorders involving aberrant protein expression or biological activity.
XX CC The polypeptide and polynucleotide sequences have applications in
XX CC diagnostics, forensics, gene mapping, identification of mutations
XX CC responsible for genetic disorders or other traits to assess biodiversity
XX CC and to produce other types of data and products dependent on DNA and
XX CC amino acid sequences. ABG00010-ABG30377 represent novel human
XX CC diagnostic amino acid sequences of the invention.
XX CC Note: The sequence data for this patent did not appear in the printed
XX CC specification, but was obtained in electronic format directly from WIPO
XX CC at ftp.wipo.int/pub/published_pct_sequences.
XX XX
XX SQ Sequence 108 AA:
XX
XX Query Match 66.1%; Score 39; DB 22; Length 108;
XX Best Local Similarity 100.0%; Pred. No. 3.2e-33;
XX Matches 39; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
```

```
OY 20 AKOEKKKKKTGAKRRMOYNRRFVNVPFGKKKGPNN 58
DB 69 AKOEKKKKKTGAKRRMOYNRRFVNVPFGKKKGPNN 107
```

```
RESULT 8
AAO08731
ID AAO08731 standard; Protein; 40 AA.
XX
XX AC AAO08731;
XX
XX DT 06-NOV-2001 (first entry)
```


XX Human polypeptide SEQ ID NO 22623.
DE
XX
KW Human: cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorders; arthritis; inflammation.
XX
OS Homo sapiens.
PN WO200164835-A2.
XX
PD 07-SEP-2001.
XX
PP 26-FEB-2001; 2001WO-US04927.
XX
PR 28-FEB-2000; 2000US-0515126.
XX 18-MAY-2000; 2000US-0577409.
PA (HYTE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI: 2001-514838/56.
XX N-PSDB; AA188662.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders.
XX
XX
PS Claim 20; SEQ ID NO 22623; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activity/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 40 AA;
XX
Query Match 62.7%; Score 37; DB 22; Length 40;
Best Local Similarity 100.0%; Pred. No. 1.7e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 EKKKKKTGRAKRRMQYRRFVNVPTFGKKKGPANNS 59
Db 4 EKKKKKTGRAKRRMQYRRFVNVPTFGKKKGPANNS 40
XX
RESULT 9
AAG75965
ID AAG75965 standard; Protein: 157 AA.
XX
AC AAG75965;
XX
DT 03-SEP-2001 (first entry)
XX
DE Human colon cancer antigen protein SEQ ID NO:6729.
XX
KW Human: colon cancer; colon cancer antigen; diagnosis; detection;
KW colorectal carcinoma; chromosome 11.
XX
OS Homo sapiens.
XX

PN WO200122920-A2.
XX
PD 05-APR-2001.
XX
PP 28-SEP-2000; 2000WO-US26524.
XX
PR 29-SEP-1999; 99US-0157137.
XX 03-NOV-1999; 99US-0163280.
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PN Ruben SM, Barash SC, Birse CE, Rosen CA;
XX
PI WPI: 2001-23357/24.
XX N-PSDB; AAH35370.
XX
DR Nucleic acids encoding 4277 human colon cancer-associated polypeptides,
DR useful for preventing, diagnosing and/or treating colorectal cancers -
XX
XX
PS Claim 11; Page 8192-8193; 9803pp; English.
XX
CC AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon
CC cancer-associated nucleic acid molecules (N) and proteins (P), where
CC the proteins are collectively known as colon cancer antigens. The colon
CC cancer antigens have cytostatic activity and can be used in gene
CC therapy and vaccine production. N and P may be used in the prevention,
CC diagnosis and treatment of diseases associated with inappropriate P
CC expression. For example, N and P may be used to treat disorders
CC associated with decreased expression by rectifying mutations or deletions
CC in a patient's genome that affect the activity of P by expressing P.
CC Inactive proteins or to supplement the patients own production of P.
CC Additionally, N may be used to produce the colon cancer-associated Ps
CC by inserting the nucleic acids into a host cell and culturing the cell
CC to express the proteins. N and P can be used in the prevention, diagnosis
CC and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204
CC and AAB77789 represent sequences used in the exemplification of the
CC present invention.
CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were
CC missing at time of publication, meaning no sequences are present for
CC SEQ ID NO:1027 to 1052, 7921 and 7922.
XX
SQ Sequence 157 AA;
XX
Query Match 62.7%; Score 37; DB 22; Length 157;
Best Local Similarity 100.0%; Pred. No. 5.7e-31;
Matches 37; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KVNGLARAGKVRGOTPKVAKOEKKKKKTGRAKRRMQ 37
Db 106 KVNGLARAGKVRGOTPKVAKOEKKKKKTGRAKRRMQ 142
XX
RESULT 10
AAG01569
ID AAG01569 standard; Protein: 130 AA.
XX
AC AAG01569;
XX
DT 06-OCT-2000 (first entry)
XX
DE Human secreted protein, SEQ ID NO: 5650.
XX
KW Human: 5' EST; expressed sequence tag; secreted protein; cDNA isolation;
KW gene therapy; chromosome mapping.
XX
OS Homo sapiens.
PN EP1033401-A2.
XX
XX 06-SEP-2000.
XX
PD 21-FEB-2000; 2000EP-0200610.
XX
XX

PR 26-FEB-1999; 9905-0122487.
XX
XX (GEST) GENSET.
XX
PI Dumas Mline Edwards J, Duclert A, Giordano J;
XX WPI: 2000-500381/45.
DR N-PSDB; AAC01575.
XX
XX New nucleic acid that is a 5' expressed sequence tag (5' EST) for
PT obtaining cDNAs and genomic DNAs that correspond to 5' ESTs and for
PI diagnostic, forensic, gene therapy and chromosome mapping procedures -
XX
XX Claim 13; SEQ ID 5650; 71pp + CD-ROM; English.
XX
XX The present sequence is a polypeptide encoded by one of a large number
CC of 5' ESTs derived from mRNAs encoding secreted proteins. The 5' ESTs
CC were prepared from total human RNAs or polyA+ RNAs derived from 30
CC different tissues. EST sequences usually correspond mainly to the 3'
CC untranslated region (UTR) of the mRNA because they are often obtained
CC from oligo-dT primed cDNA libraries. Such ESTs are not well suited for
CC isolating cDNA sequences derived from the 5' ends of mRNAs and even in
CC those cases where longer cDNA sequences have been obtained, the full 5'
CC UTR is rarely included. 5' ESTs are derived from mRNAs with intact 5'
CC ends and can therefore be used to obtain full length cDNAs and genomic
CC DNAs. 5' ESTs are also used in diagnostic, forensic, gene therapy and
CC chromosome mapping procedures. They are used to obtain upstream
CC regulatory sequences and to design expression and secretion vectors.
XX
XX Sequence 130 AA:
SQ
Query Match 54.2%; Score 32; DB 21; Length 130;
Best Local Similarity 100.0%; Pred. No. 8.6e-26;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KYHGSLARAGKVRGQTPKVAKEKKKKKTGRA 32
DB 75 KYHGSLARAGKVRGQTPKVAKEKKKKKTGRA 106
RESULT 11
AAU30872
ID AAU30872 standard; Protein: 312 AA.
XX
AC AAU30872;
XX
DT 18-DEC-2001 (first entry)
XX
XX Novel human secreted protein #1363.
DE
XX
XX Human: vaccination; gene therapy; nutritional supplement;
KW stem cell proliferation; haematopoiesis; nerve tissue regeneration;
KW immune suppression; immune stimulation; anti-inflammatory; leukemia.
XX
OS Homo sapiens.
XX
XX WO200179449-A2.
XX
XX PD 25-OCT-2001.
XX
XX PF 16-APR-2001; 2001WO-US08656.
XX
XX PR 18-APR-2000; 2000US-0552929.
XX
XX PR 26-JAN-2001; 2001US-0770160.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Tang YT, Liu C, Drmanac RT;
XX
XX WPI: 2001-611725/70.
XX
XX Nucleic acids encoding a range of human polypeptides, useful in genetic
PT vaccination, testing and therapy -
PT

XX
XX Claim 20; Page 364; 765pp; English.
XX
XX The invention relates to novel human secreted polypeptides. The
CC polypeptides and antibodies to the polypeptides are useful for
CC determining the presence of or predisposition to a disease associated
CC with altered levels of polypeptide. The polypeptides are also useful for
CC identifying agents (agonists and antagonists) that bind to them. Cells
CC expressing the proteins are useful for identifying a therapeutic agent
CC for use in treatment of a pathology related to aberrant expression or
CC physiological interactions of the polypeptide. Vectors comprising
CC the nucleic acids encoding the polypeptides and cells genetically
CC engineered to express them are also useful for producing the proteins.
CC The proteins are useful in genetic vaccination, testing and
CC therapy, and can be used as nutritional supplements. They may be used to
CC increase stem cell proliferation; to regulate haematopoiesis; and in
CC bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC immune suppression and/or stimulation; as anti-inflammatory agents; and
CC in treatment of leukemias. AAU29510-AAU3304 represent the amino acid
XX sequences of novel human secreted proteins of the invention.
XX
XX Sequence 312 AA:
SQ
Query Match 54.2%; Score 32; DB 22; Length 312;
Best Local Similarity 100.0%; Pred. No. 1.9e-25;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 23 EKKKKKTGAKRRMOYNNRFVNVVVFEGKKKG 54
DB 72 EKKKKKTGAKRRMOYNNRFVNVVVFEGKKKG 103
RESULT 12
ABG27230
ID ABG27230 standard; Protein: 61 AA.
XX
XX ABG27230;
XX
XX DT 18-FEB-2002 (first entry)
XX
XX Novel human diagnostic protein #27221.
DE
XX
XX Human: chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
XX WO200175067-A2.
XX
XX PD 11-OCT-2001.
XX
XX PF 30-MAR-2001; 2001WO-US08631.
XX
XX PR 31-MAR-2000; 2000US-0540217.
XX
XX PR 23-AUG-2000; 2000US-0649167.
XX
XX PA (HYSE-) HYSEQ INC.
XX
XX PI Drmanac RT, Liu C, Tang YT;
XX
XX WPI: 2001-639362/73.
XX
XX DR N-PSDB; AAS91417.
XX
XX New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
XX Claim 20; SEQ ID No 57589; 103pp; English.
XX
XX The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome

CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags
CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 61 AA:

Query Match 52.5%; Score 31; DB 22; Length 61;
Best Local Similarity 100.0%; Pred. No. 4.9e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 29 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 59
DB 31 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 61
|||||
RESULT 13
ABG27520
ID ABG27520 standard; Protein: 90 AA.
XX
AC ABG27520;
XX
DT 18-FEB-2002 (first entry)
XX
DE Novel human diagnostic protein #27511.
XX
KW Human; chromosome mapping; gene mapping; gene therapy; forensic;
KW food supplement; medical imaging; diagnostic; genetic disorder.
XX
OS Homo sapiens.
XX
PN WO200175067-A2.
XX
PD 11-OCT-2001.
XX
PF 30-MAR-2001; 2001WO-US08631.
XX
PR 31-MAR-2000; 2000US-0540217.
PR 23-AUG-2000; 2000US-0649167.
XX
PA (HXSE-) HXSEQ INC.
XX
PI Drmanac RT, Liu C, Tang YT;
XX
DR WPI: 2001-639362/73.
DR N-PSDB; AAS91707.
XX
PT New isolated polynucleotide and encoded polypeptides, useful in
PT diagnostics, forensics, gene mapping, identification of mutations
PT responsible for genetic disorders or other traits and to assess
PT biodiversity -
XX
PS Claim 20; SEQ ID NO 57879; 103bp; English.
XX
CC The invention relates to isolated polynucleotide (I) and
CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
CC and gene mapping, and in recombinant production of (II). The
CC polynucleotides are also used in diagnostics as expressed sequence tags

CC for identifying expressed genes. (I) is useful in gene therapy techniques
CC to restore normal activity of (II) or to treat disease states involving
CC (II). (II) is useful for generating antibodies against it, detecting or
CC quantitating a polypeptide in tissue, as molecular weight markers and as
CC a food supplement. (II) and its binding partners are useful in medical
CC imaging of sites expressing (II). (I) and (II) are useful for treating
CC disorders involving aberrant protein expression or biological activity.
CC The polypeptide and polynucleotide sequences have applications in
CC diagnostics, forensics, gene mapping, identification of mutations
CC responsible for genetic disorders or other traits to assess biodiversity
CC and to produce other types of data and products dependent on DNA and
CC amino acid sequences. ABG00010-ABG30377 represent novel human
CC diagnostic amino acid sequences of the invention.
CC Note: The sequence data for this patent did not appear in the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 90 AA:

Query Match 52.5%; Score 31; DB 22; Length 90;
Best Local Similarity 100.0%; Pred. No. 7e-25;
Matches 31; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 29 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 59
DB 60 TGRARRMQYNRRFVNVPTFGKKKGPNNNS 90
|||||
RESULT 14
ABB29449
ID ABB29449 standard; Peptide: 118 AA.
XX
AC ABB29449;
XX
DT 01-FEB-2002 (first entry)
XX
DE Peptide #2100 encoded by breast cell single exon nucleic acid probe.
XX
KW Human; microarray; single exon probe; gene expression; breast;
KW disease; cancer.
XX
OS Homo sapiens.
XX
PN WO200157271-A2.
XX
PD 09-AUG-2001.
XX
PF 30-JAN-2001; 2001WO-US00662.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI: 2001-496933/54.
XX
PT New spatially-addressable set of single exon nucleic acid probes,
PT useful for measuring gene expression in sample derived from human
PT breast, comprises number of single exon nucleic acid probes -
XX
PS Claim 27; SEQ ID NO 12417; 327bp + sequence listing; English.
XX
CC The invention relates to a spatially-addressable set of single exon
CC nucleic acid probes for measuring gene expression in a sample derived
CC from human breast and BT 474 cells. The method involves contacting
CC the probes with a collection of detectably labelled nucleic acids

CC derived from mRNA of human breast, and then measuring the label
CC bound to each probe of the microarray. The probes are useful for
CC verifying the expression of regions of genomic DNA predicted to
CC determine proteins. They are useful for gene discovery, and for
CC determining predisposition and/or prognosing breast disease. Gene
CC expression analysis is useful for assessing the toxicity of chemical
CC agents on cells. The microarray of this invention presents a far greater
CC diversity of probes for measuring gene expression, with far less bias
CC than expressed sequence tag microarrays. The method is suitable for
CC rapid production of functional information from genomic sequence. The
CC present sequence is a peptide encoded by a single exon nucleic acid
CC probe of the invention.
CC Note: The sequence data for this patent did not form part of the
CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHSLARAGKVRGOTPRVAKOEKKKK 28
Db 56 KVHSLARAGKVRGOTPRVAKOEKKKK 83

RESULT 15
ABB34625
ID ABB34625 standard; Peptide: 118 AA.
XX
AC ABB34625;
XX
DT 04-FEB-2002 (first entry)
XX
DE Peptide #2131 encoded by human foetal liver single exon probe.
XX
KW Human; foetal liver; gene expression; single exon nucleic acid probe.
XX
OS Homo sapiens.
XX
PN WO200157277-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00669.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-483447/52.
XX
PT Human genome-derived single exon nucleic acid probes useful for
XX analyzing gene expression in human foetal liver.
XX
XX
XX Claim 27; SEQ ID NO 27260; 639pp + sequence listing; English.
XX
XX The invention relates to a single exon nucleic acid probe for
XX measuring human gene expression in a sample derived from human foetal
XX liver. The single exon nucleic acid probes may be used for predicting,
XX measuring and displaying gene expression in samples derived from human
XX foetal liver. The present sequence is a peptide encoded by a single exon
XX nucleic acid probe of the invention.
CC Note: The sequence data for this patent did not form part of the

CC printed specification, but was obtained in electronic format directly
CC from WIPO at ftp.wipo.int/pub/published_pct_sequences.
CC
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHSLARAGKVRGOTPRVAKOEKKKK 28
Db 56 KVHSLARAGKVRGOTPRVAKOEKKKK 83

RESULT 16
ABB20035
ID ABB20035 standard; Protein: 118 AA.
XX
AC ABB20035;
XX
DT 23-JAN-2002 (first entry)
XX
DE Protein #2034 encoded by probe for measuring heart cell gene expression.
XX
KW Human; gene expression; heart; microarray; vascular system;
KW cardiovascular disease; hypertension; cardiac arrhythmia;
KW congenital heart disease.
XX
OS Homo sapiens.
XX
PN WO200157274-A2.
XX
PD 09-AUG-2001.
XX
PE 30-JAN-2001; 2001WO-US00666.
XX
PR 04-FEB-2000; 2000US-0180312.
PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX
PA (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488899/53.
XX
PT Single exon nucleic acid probes for analyzing gene expression in human
XX hearts -
XX
XX
XX Claim 15; SEQ ID NO 21805; 530pp; English.
XX
XX The present invention relates to single exon nucleic acid probes for
XX measuring human gene expression in a sample derived from human heart (see
XX CC ABA21535-ABA41305). The present sequence is a protein encoded by one such
XX probe. The probes may be used for predicting, measuring and displaying
XX gene expression in samples derived from the human heart via microarrays.
XX By measuring gene expression, the probes are useful for predicting,
XX diagnosing, grading, staging, monitoring and prognosing diseases of the
XX human heart and vascular system e.g. cardiovascular disease,
XX hypertension, cardiac arrhythmias and congenital heart disease.
XX Note: The sequence data for this patent did not form part of the printed
XX specification, but was obtained in electronic format directly from WIPO
XX at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

PR 26-MAY-2000; 2000US-0207456.
PR 30-JUN-2000; 2000US-0608408.
PR 03-AUG-2000; 2000US-0632366.
PR 21-SEP-2000; 2000US-0234687.
PR 27-SEP-2000; 2000US-0236359.
PR 04-OCT-2000; 2000GB-0024263.
XX
XX (MOLE-) MOLECULAR DYNAMICS INC.
XX
PI Penn SG, Hanzel DK, Chen W, Rank DR;
XX
DR WPI; 2001-488901/53.
XX
PT Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human cervical epithelial cells -
XX
PS Claim 27; SEQ ID No 20446; 487pp; English.
XX
XX The present invention relates to human single exon nucleic acid probes
CC (SENP: see A110068-A1128459). The present sequence is a peptide encoded
CC by one such probe. The SENPs are derived from human Hela cells. The SENPs
CC can be used to produce a single exon microarray, which can be used for
CC measuring human gene expression in a sample derived from human cervical
CC epithelial cells. By measuring gene expression, the probes are therefore
CC useful in grading and/or staging of diseases of the cervix, notably
CC cervical cancer.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKHGSLARAGKVGQTPPKVAKOEKKKK 28
DB 56 KKHGSLARAGKVGQTPPKVAKOEKKKK 83

RESULT 20

ID AAM28118 standard; Protein; 118 AA.

XX AAM28118;

DT 17-OCT-2001 (first entry)

XX Peptide #2155 encoded by probe for measuring placental gene expression.

KW Probe: microarray; human; placenta; antenatal diagnosis;
KW genetic disorder.

OS Homo sapiens.

XX WO200157272-A2.

PD 09-AUG-2001.

PF 30-JAN-2001; 2001WO-US00663.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

XX WPI; 2001-48897/53.
XX
XX Human genome-derived single exon nucleic acid probes useful for
PT analyzing gene expression in human placenta -
XX
XX Claim 27; SEQ ID No 28387; 654pp; English.
XX
XX The present invention relates to single exon nucleic acid probes (SENP;
CC see A1131315-A1157546). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for producing a microarray for
CC predicting, measuring and displaying gene expression in samples derived
CC from human placenta. The probes are useful for antenatal diagnosis of
CC human genetic disorders.

SQ Sequence 118 AA;

Query Match 47.5%; Score 28; DB 22; Length 118;
Best Local Similarity 100.0%; Pred. No. 1.3e-21;
Matches 28; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKHGSLARAGKVGQTPPKVAKOEKKKK 28
DB 56 KKHGSLARAGKVGQTPPKVAKOEKKKK 83

RESULT 21

ID AAM03364 standard; Protein; 118 AA.

XX AAM03364;

DT 09-OCT-2001 (first entry)

XX Peptide #2046 encoded by probe for measuring breast gene expression.

KW Probe: human; breast disease; breast cancer; development disorder;
KW inflammatory disease; proliferative breast disease; non-carcinoma tumour.

OS Homo sapiens.

XX WO200157270-A2.

PD 09-AUG-2001.

PF 29-JAN-2001; 2001WO-US00661.

XX 04-FEB-2000; 2000US-0180312.

PR 26-MAY-2000; 2000US-0207456.

PR 30-JUN-2000; 2000US-0608408.

PR 03-AUG-2000; 2000US-0632366.

PR 21-SEP-2000; 2000US-0234687.

PR 27-SEP-2000; 2000US-0236359.

PR 04-OCT-2000; 2000GB-0024263.

XX (MOLE-) MOLECULAR DYNAMICS INC.

PA Penn SG, Hanzel DK, Chen W, Rank DR;

DR WPI; 2001-476286/51.

XX Novel single exon nucleic acid probe used to measuring gene expression

PT in a human breast -

XX Claim 27; SEQ ID No 12104; 322pp; English.

XX The present invention relates to novel single exon nucleic acid probes
CC (see A1100010-A110067). The present sequence is a peptide encoded by one
CC such probe. The probes are useful for measuring human gene expression in
CC a human breast sample, where the probe hybridises at high stringency to a
CC nucleic acid expressed in the human breast. The probes are useful for
CC predicting, diagnosing, grading, staging, monitoring and prognosing
CC diseases of the human breast, particularly those diseases with polygenic

XX WPI; 2001-514838/56.
DR N-PSDB; AA187044.
XX
PT Isolated nucleic acids and polypeptides, useful for preventing
PT diagnosing and treating e.g. leukaemia, inflammation and immune
PT disorders -
XX
PS Claim 20; SEQ ID NO 21005; 1399pp + Sequence Listing; English.
XX
CC The invention relates to human polynucleotides (AA179941-AA193841) and
CC the encoded proteins (AA000010-AA013910) that exhibit activity relating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation.
CC Note: The sequence data for this patent did not form part of the printed
CC specification, but was obtained in electronic format directly from WIPO
CC at ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 35 AA:

Query Match 40.7%; Score 24; DB 22; Length 35;
Best Local Similarity 100.0%; Pred. No. 6.8e-18;
Matches 24; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 36 MOYRRRFVNVVPPFGKKKGPNANS 59
DB 12 MOYRRRFVNVVPPFGKKKGPNANS 35

RESULT 24
AAG04311
ID AAG04311 standard; Protein; 62 AA.
XX
AC AAG04311;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 290.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 99US-0131449.

PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
PR 06-MAY-1999; 99US-0132486.
PR 06-MAY-1999; 99US-0132487.
PR 07-MAY-1999; 99US-0132863.
PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
PR 14-MAY-1999; 99US-0134219.
PR 14-MAY-1999; 99US-0134221.
PR 14-MAY-1999; 99US-0134270.
PR 18-MAY-1999; 99US-0134768.
PR 19-MAY-1999; 99US-0134941.
PR 20-MAY-1999; 99US-0135124.
PR 21-MAY-1999; 99US-0135353.
PR 24-MAY-1999; 99US-0135629.
PR 25-MAY-1999; 99US-0136021.
PR 27-MAY-1999; 99US-0136392.
PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
PR 04-JUN-1999; 99US-0137502.
PR 07-JUN-1999; 99US-0137724.
PR 08-JUN-1999; 99US-0138094.
PR 10-JUN-1999; 99US-0138540.
PR 10-JUN-1999; 99US-0138847.
PR 14-JUN-1999; 99US-0139119.
PR 16-JUN-1999; 99US-0139452.
PR 16-JUN-1999; 99US-0139453.
PR 17-JUN-1999; 99US-0139492.
PR 18-JUN-1999; 99US-0139454.
PR 18-JUN-1999; 99US-0139455.
PR 18-JUN-1999; 99US-0139456.
PR 18-JUN-1999; 99US-0139457.
PR 18-JUN-1999; 99US-0139458.
PR 18-JUN-1999; 99US-0139459.
PR 18-JUN-1999; 99US-0139460.
PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
PR 18-JUN-1999; 99US-0139763.
PR 21-JUN-1999; 99US-0139817.
PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.
PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
PR 13-JUL-1999; 99US-0143542.
PR 14-JUL-1999; 99US-0143624.
PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
PR 16-JUL-1999; 99US-0144086.
PR 19-JUL-1999; 99US-0144325.
PR 19-JUL-1999; 99US-0144331.
PR 19-JUL-1999; 99US-0144332.
PR 19-JUL-1999; 99US-0144333.
PR 19-JUL-1999; 99US-0144334.
PR 19-JUL-1999; 99US-0144335.
PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
PR 20-JUL-1999; 99US-0144884.
PR 21-JUL-1999; 99US-0144814.

PR 21-JUL-1999; 99US-0145086.
PR 21-JUL-1999; 99US-0145088.
PR 22-JUL-1999; 99US-0145085.
PR 22-JUL-1999; 99US-0145087.
PR 22-JUL-1999; 99US-0145089.
PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.
PR 23-JUL-1999; 99US-0145218.
PR 23-JUL-1999; 99US-0145224.
PR 26-JUL-1999; 99US-0145226.
PR 27-JUL-1999; 99US-0145913.
PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
PR 02-AUG-1999; 99US-0146389.
PR 03-AUG-1999; 99US-0147038.
PR 04-AUG-1999; 99US-0147204.
PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149920.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158022.
PR 08-OCT-1999; 99US-0158222.
PR 12-OCT-1999; 99US-0158369.
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PR 21-OCT-1999; 99US-0160741.
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PR 22-OCT-1999; 99US-0160981.
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PR 25-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Caps 0;

Qy 1 KVHGSRLARACKVRCGOTPRVAKO 22
Db 3 KVHGSRLARACKVRCGOTPRVAKO 24

RESULT 25
AAG15348
ID AAG15348 standard; Protein: 62 AA.
XX
AC AAG15348;
XX
DT 17-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 15567.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.

OS Arabidopsis thaliana.
XX
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126284.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130449.
PR 23-APR-1999; 99US-0130510.
PR 28-APR-1999; 99US-0130891.
PR 30-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
PR 30-APR-1999; 99US-0132407.
PR 04-MAY-1999; 99US-0132484.
PR 05-MAY-1999; 99US-0132485.
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PR 11-MAY-1999; 99US-0134256.
PR 14-MAY-1999; 99US-0134218.
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PR 27-MAY-1999; 99US-0136392.
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PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 30-JUN-1999; 99US-0141287.
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PR 22-JUL-1999; 99US-0145192.
PR 23-JUL-1999; 99US-0145145.

PR 23-JUL-1999; 99US-0145218.
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PR 27-JUL-1999; 99US-0145919.
PR 28-JUL-1999; 99US-0145951.
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PR 04-AUG-1999; 99US-0147302.
PR 05-AUG-1999; 99US-0147192.
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PR 06-AUG-1999; 99US-0147303.
PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
PR 09-AUG-1999; 99US-0147935.
PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
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PR 20-AUG-1999; 99US-0149722.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151348.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.38; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVHSLARAGKVRGOTPRVAKQ 22
Db 3 KVHSLARAGKVRGOTPRVAKQ 24

RESULT 26
AAG22753
ID AAG22753 standard; Protein; 62 AA.
XX
AC AAG22753;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 25803.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
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PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
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PR 28-JUL-1999; 99US-0145951.

PR 02-AUG-1999; 99US-0146386.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 20-AUG-1999; 99US-0149722.
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PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
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PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 06-OCT-1999; 99US-0157865.
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PR 08-OCT-1999; 99US-0158232.
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PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSLRAGKVRGQTPKYAKQ 22
Db 3 KVHGSLRAGKVRGQTPKYAKQ 24

RESULT 27
AACG32888
ID AACG32888 standard; Protein: 62 AA.
AC AACG32888;
XX
XX
DT 17-OCT-2000 (first entry)
XX
XX Zea mays protein fragment SEQ ID NO: 39761.
DE
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
XX EP1033405-A2.
PN
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
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PR 07-JUN-1999; 99US-0137724.
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PR 14-JUN-1999; 99US-0138847.
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PR 18-JUN-1999; 99US-0139460.
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Query Match

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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%: Score 22; DB 21; length 62;
Best Local Similarity 100.0%: Pred. No. 14e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 3 KVHGSILRAGKVRGOTPRVAKO 24

RESULT 29
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AC AAG38861;
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DT 18-OCT-2000 (first entry)
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DE Arabidopsis thaliana protein fragment SEQ ID NO: 48004.
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KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1,4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KKHGSLARAGKVRGOTPKVAKO 22
DB 3 KKHGSLARAGKVRGOTPKVAKO 24

RESULT 30
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AC AAG39476;
XX

DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 48848.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KM hydrolisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
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PE 25-FEB-2000; 2000EP-0301439.
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Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred No. 1.4e-15;
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QY 1 KVGSLARAGKVRGQTPPKAKQ 22
Db 3 KVGSLARAGKVRGQTPPKAKQ 24

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AC AAG40704;

DT 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 50541.

DE Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.
OS
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PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1,4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARAGKVRGQTPKVAKO 22
Db 3 KVHSLARAGKVRGQTPKVAKO 24

RESULT 32
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AC AAG40788;
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DT 18-OCT-2000 (first entry)
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DE Zea mays protein fragment SEQ ID NO: 50657.
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KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
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OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
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PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 26-OCT-1999; 99US-0161360.
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PR 28-OCT-1999; 99US-0161982.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1.4e-15;

Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSRLARACKVRCGTPPVAKQ 22
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Db 3 KVHGSRLARACKVRCGTPPVAKQ 24

RESULT 33

AAG44883
ID AAG44883 standard; Protein: 62 AA.

XX AAG44883;

XX 18-OCT-2000 (first entry)

XX Zea mays protein fragment SEQ ID NO: 56275.

KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.

XX Zea mays subsp. mays.

XX EPI033405-A2.

XX 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 03-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

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PR 04-MAY-1999; 99US-0132484.
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PR 28-MAY-1999; 99US-0136782.
PR 01-JUN-1999; 99US-0137222.
PR 03-JUN-1999; 99US-0137528.
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PR 07-JUN-1999; 99US-0137724.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.38; Score 22; DB 21; Length 62;
Best Local Similarity 100.0%; Pred. No. 1,4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHSLARAGKVRGQTPKVKAKO 22
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Db 3 KVHSLARAGKVRGQTPKVKAKO 24

RESULT 34
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ID AAC48690 standard; protein; 62 AA.
XX
AC AAC48690;
XX
DT 18-OCT-2000 (first entry)
XX
DE Arabidopsis thaliana protein fragment SEQ ID NO: 61514.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence.
XX
OS Arabidopsis thaliana.
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
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PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161992.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match Best Local Similarity 37.3%; Score 22; DB 21; Length 62;
Matches 22; Conservative 100.0%; Pred. No. 1,4e-15; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHSLARAGKVRGOTPRVAKO 22
Db 3 KVHSLARAGKVRGOTPRVAKO 24
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RESULT 35
AAG31871
ID AAG31871 standard; Protein: 68 AA.

AC AAG31871;

XX 17-OCT-2000 (first entry)

DE Arabidopsis thaliana protein fragment SEQ ID NO: 38348.

KW Protein identification; signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.

OS Arabidopsis thaliana.

PN EP1033405-A2.

XX EP1033405-A2.

PD 06-SEP-2000.

PF 25-FEB-2000; 2000EP-0301439.

XX 25-FEB-1999; 99US-0121825.

PR 05-MAR-1999; 99US-0123180.

PR 09-MAR-1999; 99US-0123548.

PR 23-MAR-1999; 99US-0125788.

PR 25-MAR-1999; 99US-0126264.

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PR 26-OCT-1999; 99US-0161361.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 68;
Best Local Similarity 100.0%; Pred. No. 1,5e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 KVHGSLLARAGKVRGQTPKVAKO 22
Db 9 KVHGSLLARAGKVRGQTPKVAKO 30
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RESULT 36
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ID AAG40703 standard; Protein; 82 AA.
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AC AAG40703;
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DT 18-OCT-2000 (first entry)
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DE Zea mays protein fragment SEQ ID NO: 50540.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
OS
XX
PN EP1033405-A2.
XX
PD 06-SEP-2000.
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XX
PF 25-FEB-2000; 2000EP-0301439.
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PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 29-MAR-1999; 99US-0126785.
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PR 06-APR-1999; 99US-0128234.
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PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 82;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 KVHSLARAGVRCGTPEVAKO 22
Db 23 KVHSLARAGVRCGTPEVAKO 44
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ID AAG44882 standard; Protein; 83 AA.
AC AAG44882;
XX 18-OCT-2000 (first entry)
DT Zea mays protein fragment SEQ ID NO: 56274.
XX
DE Zea mays protein fragment SEQ ID NO: 56274.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EPI033405-A2.
XX
PD 06-SEP-2000.
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PF 25-FEB-2000; 2000EP-0301439.
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PR 22-OCT-1999; 99US-0160989.
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PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.

PR 29-OCT-1999; 99US-0162142.
Query Match 37.3%; Score 22; DB 21; Length 83;
Best Local Similarity 100.0%; Pred. No. 1.8e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 24 KVGSLARAGKVRGQTPRYAKQ 45
RESULT 38
AAG3287
ID AAG3287 standard; Protein: 84 AA.
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AC AAG3287;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 39760.
XX
KW Protein identification; signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EPI033405-A2.
PN
PD 06-SEP-2000.
XX
PE 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
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PR 30-APR-1999; 99US-0132048.
PR 04-MAY-1999; 99US-0132407.
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PR 06-MAY-1999; 99US-0132486.
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PR 28-MAY-1999; 99US-0136782.
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PR 04-JUN-1999; 99US-0137502.
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PR 08-JUN-1999; 99US-0138094.

PR 10-JUN-1999; 99US-0138540.
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PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 84;
Best Local Similarity 100.0%; Pred. No. 1.9e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 KKHGSLRACKVKQPTKVAQ 22

Db 25 KVGSLRAGKVRGQTPKVAQ 46
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RESULT 39
AAG34118
ID AAG34118 standard; Protein: 93 AA.
XX
AC AAG34118;
XX
DT 18-OCT-2000 (first entry)
DE Zea mays protein fragment SEQ ID NO: 41465.
XX
XX Protein identification: signal transduction pathway: metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP103405-A2.
XX
PD 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
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PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
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PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.38; Score 22; DB 21; Length 93;
Best Local Similarity 100.08; Pred. No. 2e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 KVHSLARAGKVRGQTPRVAKQ 22
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Db 34 KVHSLARAGKVRGQTPRVAKQ 55

RESULT 40
AAG32886
ID AAG32886 standard; Protein: 110 AA.

XX
AC AAG32886;
XX
DT 17-OCT-2000 (first entry)
XX
DE Zea mays protein fragment SEQ ID NO: 39759.
XX
KW Protein identification: signal transduction pathway; metabolic pathway;
KW hybridisation assay; genetic mapping; gene expression control; promoter;
KW termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
PN EP1033405-A2.
PD
XX 06-SEP-2000.
XX
PF 25-FEB-2000; 2000EP-0301439.
XX
PR 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123180.
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PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142820.
PR 12-JUL-1999; 99US-0142877.
PR 13-JUL-1999; 99US-0143542.
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PR 28-JUL-1999; 99US-0145951.
PR 02-AUG-1999; 99US-0146386.
PR 02-AUG-1999; 99US-0146388.
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PR 04-AUG-1999; 99US-0147204.
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PR 05-AUG-1999; 99US-0147192.
PR 05-AUG-1999; 99US-0147260.
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PR 06-AUG-1999; 99US-0147416.
PR 09-AUG-1999; 99US-0147493.
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PR 10-AUG-1999; 99US-0148171.
PR 11-AUG-1999; 99US-0148319.
PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148565.
PR 13-AUG-1999; 99US-0148684.
PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
PR 18-AUG-1999; 99US-0149426.
PR 20-AUG-1999; 99US-0149722.
PR 20-AUG-1999; 99US-0149723.
PR 20-AUG-1999; 99US-0149929.
PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.

PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
PR 27-AUG-1999; 99US-0151066.
PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.
PR 01-SEP-1999; 99US-0151930.
PR 07-SEP-1999; 99US-0152363.
PR 10-SEP-1999; 99US-0153070.
PR 13-SEP-1999; 99US-0153758.
PR 15-SEP-1999; 99US-0154018.
PR 16-SEP-1999; 99US-0154039.
PR 20-SEP-1999; 99US-0154779.
PR 22-SEP-1999; 99US-0155139.
PR 23-SEP-1999; 99US-0155486.
PR 24-SEP-1999; 99US-0155659.
PR 28-SEP-1999; 99US-0156458.
PR 29-SEP-1999; 99US-0156596.
PR 04-OCT-1999; 99US-0157117.
PR 05-OCT-1999; 99US-0157753.
PR 06-OCT-1999; 99US-0157865.
PR 07-OCT-1999; 99US-0158029.
PR 08-OCT-1999; 99US-0158232.
PR 12-OCT-1999; 99US-0158369.
PR 13-OCT-1999; 99US-0159293.
PR 13-OCT-1999; 99US-0159294.
PR 13-OCT-1999; 99US-0159295.
PR 14-OCT-1999; 99US-0159325.
PR 14-OCT-1999; 99US-0159330.
PR 14-OCT-1999; 99US-0159331.
PR 14-OCT-1999; 99US-0159637.
PR 14-OCT-1999; 99US-0159638.
PR 18-OCT-1999; 99US-0159584.
PR 21-OCT-1999; 99US-0160741.
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PR 21-OCT-1999; 99US-0160815.
PR 22-OCT-1999; 99US-0160980.
PR 22-OCT-1999; 99US-0160981.
PR 22-OCT-1999; 99US-0160989.
PR 22-OCT-1999; 99US-0161404.
PR 25-OCT-1999; 99US-0161405.
PR 25-OCT-1999; 99US-0161406.
PR 26-OCT-1999; 99US-0161359.
PR 26-OCT-1999; 99US-0161360.
PR 26-OCT-1999; 99US-0161361.
PR 28-OCT-1999; 99US-0161920.
PR 28-OCT-1999; 99US-0161922.
PR 28-OCT-1999; 99US-0161993.
PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 110;
Best Local Similarity 100.0%; Pred. No. 2,4e-15;
Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KKHGSLARAGKVRGQTPKVAQ 22
DB 51 KKHGSLARAGKVRGQTPKVAQ 72

RESULT 41

AAG26728
ID AAG26728 standard; Protein; 130 AA.

XX AAG26728;

XX 17-OCT-2000 (first entry)

DT Zea mays protein fragment SEQ ID NO: 31293.

XX

KW Protein identification: signal transduction pathway; metabolic pathway;
KM hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence; corn.
XX
OS Zea mays subsp. mays.
XX
XX EPI033405-A2.
PN
XX
PD 06-SEP-2000.
XX
XX 25-FEB-2000; 2000EP-0301439.
PF
XX
XX 25-FEB-1999; 99US-0121825.
PR 05-MAR-1999; 99US-0123380.
PR 09-MAR-1999; 99US-0123548.
PR 23-MAR-1999; 99US-0125788.
PR 25-MAR-1999; 99US-0126264.
PR 29-MAR-1999; 99US-0126785.
PR 01-APR-1999; 99US-0127462.
PR 06-APR-1999; 99US-0128234.
PR 08-APR-1999; 99US-0128714.
PR 16-APR-1999; 99US-0129845.
PR 19-APR-1999; 99US-0130077.
PR 21-APR-1999; 99US-0130510.
PR 23-APR-1999; 99US-0130891.
PR 28-APR-1999; 99US-0131449.
PR 30-APR-1999; 99US-0132048.
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PR 05-MAY-1999; 99US-0132485.
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PR 14-MAY-1999; 99US-0134370.
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PR 01-JUN-1999; 99US-0137222.
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PR 18-JUN-1999; 99US-0139461.
PR 18-JUN-1999; 99US-0139462.
PR 18-JUN-1999; 99US-0139463.
PR 18-JUN-1999; 99US-0139750.
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PR 22-JUN-1999; 99US-0139899.
PR 23-JUN-1999; 99US-0140353.

PR 23-JUN-1999; 99US-0140354.
PR 24-JUN-1999; 99US-0140695.
PR 28-JUN-1999; 99US-0140823.
PR 29-JUN-1999; 99US-0140991.
PR 30-JUN-1999; 99US-0141287.
PR 01-JUL-1999; 99US-0141842.
PR 01-JUL-1999; 99US-0142154.
PR 02-JUL-1999; 99US-0142055.
PR 06-JUL-1999; 99US-0142390.
PR 08-JUL-1999; 99US-0142803.
PR 09-JUL-1999; 99US-0142920.
PR 12-JUL-1999; 99US-0142977.
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PR 15-JUL-1999; 99US-0144005.
PR 16-JUL-1999; 99US-0144085.
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PR 19-JUL-1999; 99US-0144325.
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PR 20-JUL-1999; 99US-0144352.
PR 20-JUL-1999; 99US-0144632.
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PR 22-JUL-1999; 99US-0145087.
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PR 12-AUG-1999; 99US-0148341.
PR 13-AUG-1999; 99US-0148365.
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PR 16-AUG-1999; 99US-0149368.
PR 17-AUG-1999; 99US-0149175.
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PR 23-AUG-1999; 99US-0149902.
PR 23-AUG-1999; 99US-0149930.
PR 25-AUG-1999; 99US-0150566.
PR 26-AUG-1999; 99US-0150884.
PR 27-AUG-1999; 99US-0151065.
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PR 27-AUG-1999; 99US-0151080.
PR 30-AUG-1999; 99US-0151303.
PR 31-AUG-1999; 99US-0151438.

PR 01-SEP-1999; 99US-0151930.
 PR 07-SEP-1999; 99US-0152363.
 PR 10-SEP-1999; 99US-0153070.
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 PR 07-OCT-1999; 99US-0158029.
 PR 08-OCT-1999; 99US-0158232.
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 PR 22-OCT-1999; 99US-0160880.
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 PR 25-OCT-1999; 99US-0161404.
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 PR 25-OCT-1999; 99US-0161406.
 PR 26-OCT-1999; 99US-0161359.
 PR 26-OCT-1999; 99US-0161360.
 PR 26-OCT-1999; 99US-0161361.
 PR 28-OCT-1999; 99US-0161920.
 PR 28-OCT-1999; 99US-0161922.
 PR 28-OCT-1999; 99US-0161993.
 PR 29-OCT-1999; 99US-0162142.

Query Match 37.3%; Score 22; DB 21; Length 130;
 Best Local Similarity 100.0%; Pred. No. 2.7e-15;
 Matches 22; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 KVGSLRAGKVRGQTPKVAQ 22
 DB 71 KVGSLRAGKVRGQTPKVAQ 92

RESULT 42
 ABG34133

ID ABG34133 standard; Protein: 230 AA.

AC ABG34133;

DT 15-JUL-2002 (first entry)

DE Human seb4B protein.

XX Tax interacting protein clone 2; TIP-2; GIPC; antigen; tumour;
 KW breast cancer; prostate cancer; monoclonal antibody; 27.B1; 27.F7;
 KW thyroid cancer; tetanus toxin; infection; HIV; hanta virus; Ebola;
 KW human immunodeficiency virus infection; enzyme dysfunction;
 KW hormone dysfunction; autoimmune disease; lupus; rheumatoid arthritis;
 KW Immune dysfunction; septicemia; human.
 XX

OS Homo sapiens.
 XX
 PN WO200222851-A2.
 XX
 PD 21-MAR-2002.
 XX
 XX
 PF 18-SEP-2001; 2001WO-US29242.
 XX
 PR 18-SEP-2000; 2000US-0664958.
 XX
 PA (UYCO) UNIV COLUMBIA NEW YORK.
 XX
 PI Trakht I, Canfield R, Kalantarov G, Rudchenko S;
 DR WPI: 2002-362353/39.
 XX N-PSDB; ABK70029.
 XX
 PT New monoclonal antibody which specifically binds and forms complex with
 PT TIP-2 antigen located on surface of human cancer cells, useful for
 PT diagnosing and treating cancer in a human subject -
 XX
 PS Example 6; Fig 41B; 276pp; English.

XX The invention relates to a monoclonal (mab) antibody which specifically
 CC binds and forms a complex with TIP-2 (Tax interacting protein clone 2,
 CC also known as GIPC) antigen located on the surface of human cancer cells,
 CC where mab binds to the same antigen as monoclonal antibody 27.B1
 CC or 27.F7 produced by hybridoma 27.B1 or 27.F7 of ATCC Designation No.
 CC PTA-1599 or 1598, respectively. The mab is useful for detecting TIP-2
 CC antigen bearing cancer cells, for diagnosing cancer in a subject by
 CC detecting TIP-2 antigen-bearing cancer cells, for in vivo diagnosis of
 CC cancer in a subject, for delivering exogenous material to TIP-2 antigen-
 CC bearing cancer cells of a human subject, for treating cancer in a human
 CC subject, for inducing apoptosis of a tissue section from a tumour sample
 CC for the presence of TIP-2 antigen bearing cancer cells, for detecting the
 CC presence of TIP-2 antigen in biological fluid, and for monitoring the
 CC progression of cancer, where the cancer cells are TIP-2 antigen-bearing
 CC cancer cells, in a subject. A composition comprising the mab is useful
 CC for treating or preventing a condition in a subject who previously
 CC exhibited the condition, where the condition is associated with cancer
 CC (thyroid, breast or prostate cancer), tumour (benign), toxin (tetanus,
 CC anthrax, botulinum, snake venom or spider venom), infectious agent (such
 CC as Hanta virus, HTLV (not defined) I, HTLV II, Human immunodeficiency
 CC virus, HIV herpes virus, influenza, Ebola, human papilloma virus,
 CC Staphylococcus, Streptococcus, Klebsiella, Escherichia coli, anthrax or
 CC Cryptococcus), enzyme dysfunction (hyperactivity or overproduction of the
 CC enzyme), hormone dysfunction (hyperactivity or overproduction of the
 CC hormone), autoimmune disease (lupus, thyroiditis, graft versus host
 CC disease, transplantation rejection or rheumatoid arthritis), immune
 CC dysfunction (CD3 or CD4 mediated), viral antigen, bacterial antigen,
 CC eukaryotic antigen, rejection of a transplanted tissue, or the condition
 CC is septicemia, sepsis, septic shock, viraemia, bacteraemia, fungaemia.
 CC The present sequence is an additional human cancer associated marker
 CC which can be used in the production of monoclonal antibodies.
 XX

SO Sequence 230 AA:

Query Match 35.6%; Score 21; DB 23; Length 230;
 Best Local Similarity 100.0%; Pred. No. 5.1e-14;
 Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 RRMQVNRFRVNVPTFGKKKG 54

DB 1 RRMQVNRFRVNVPTFGKKKG 21

RESULT 43
 ABG34132

ID ABG34132 standard; Protein: 459 AA.

AC ABG34132;

XX

DT 15-JUL-2002 (first entry)
XX
DE Human seb4d protein.
XX
KW Tax interacting protein clone 2; TIP-2; GIPC; antigen; tumour;
KW breast cancer; prostate cancer; monoclonal antibody; 27.B1; 27.F7;
KW thyroid cancer; tetanus toxin; infection; HIV; hanta virus; Ebola;
KW human immunodeficiency virus infection; enzyme dysfunction;
KW hormone dysfunction; autoimmune disease; lupus; rheumatoid arthritis;
KW immune dysfunction; septicemia; human.
XX
OS Homo sapiens.
XX
PN MO20022851-A2.
XX
PD 21-MAR-2002.
XX
PF 18-SEP-2001; 2001WO-US29242.
XX
PR 18-SEP-2000; 2000US-0664958.
XX
XX (UYCO) UNIV COLUMBIA NEW YORK.
XX
PI Trakht I, Canfield R, Kalantarov G, Rudchenko S;
XX
DR WPI; 2002-362353/39.
XX
DR N-PSDB; ABR70028.
XX
PT New monoclonal antibody which specifically binds and forms complex with
PT TIP-2 antigen located on surface of human cancer cells, useful for
PT diagnosing and treating cancer in a human subject -
XX
XX
PS Example 6; Fig 41A; 276pp; English.
XX
XX The invention relates to a monoclonal (mab) antibody which specifically
XX binds and forms a complex with TIP-2 (Tax interacting protein clone 2,
XX also known as GIPC) antigen located on the surface of human cancer cells,
XX where mab binds to the same antigen as monoclonal antibody 27.B1
XX or 27.F7 produced by hybridoma 27.B1 or 27.F7 of ATCC Designation No.
XX PRA-1599 or 1598, respectively. The mab is useful for detecting TIP-2
XX antigen bearing cancer cells, for diagnosing cancer in a subject by
XX detecting TIP-2 antigen-bearing cancer cells, for in vivo diagnosis of
XX cancer in a subject, for delivering exogenous material to TIP-2 antigen-
XX bearing cancer cells of a human subject, for treating cancer in a human
XX subject, for inducing apoptosis of TIP-2 antigen bearing cells, for
XX immunohistochemical screening of a tissue section from a tumour sample
XX for the presence of TIP-2 antigen bearing cancer cells, for detecting the
XX presence of TIP-2 antigen in biological fluid, and for monitoring
XX progression of cancer, where the cancer cells are TIP-2 antigen-bearing
XX cancer cells, in a subject. A composition comprising the mab is useful
XX for treating or preventing a condition in a subject who previously
XX exhibited the condition, where the condition is associated with cancer
XX (thyroid, breast or prostate cancer), tumour (benign), toxin (tetanus,
XX anthrax, botulinum, snake venom or spider venom), infectious agent (such
XX as Hanta virus, HTLV (not defined) I, HTLV II, Human immunodeficiency
XX virus, HIV herpes virus, influenza, Ebola, human papilloma virus,
XX Staphylococcus, Streptococcus, Klebsiella, Escherichia coli, anthrax or
XX Cryptococcus), enzyme dysfunction (hyperactivity or overproduction of the
XX enzyme), hormone dysfunction (hyperactivity or overproduction of the
XX hormone), autoimmune disease (lupus, thyroiditis, graft versus host
XX disease, transplantation rejection or rheumatoid arthritis), immune
XX dysfunction (CD3 or CD4 mediated), viral antigen, bacterial antigen,
XX eukaryotic antigen, rejection of a transplanted tissue, or the condition
XX is septicemia, sepsis, septic shock, viraemia, bacteraemia, fungaemia.
XX The present sequence is an additional human cancer associated marker
XX which can be used in the production of monoclonal antibodies.
XX
XX Sequence 459 AA:
XX
XX Query Match 35.6%; Score 21; DB 23; Length 459;
XX Best Local Similarity 100.0%; Pred. No. 9, 3e-14;
XX Matches 21; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 34 RRMQYNRRFVNVVPTFGKKG 54
XX |||||||||||||||
DB 230 RRMQYNRRFVNVVPTFGKKG 250
XX
AC RESULT 44
XX AAG20231
XX ID AAG20231 standard; Protein; 65 AA.
XX
XX AAG20231;
XX
XX 17-OCT-2000 (first entry)
XX
XX Arabidopsis thaliana, protein fragment SEQ ID NO: 22339.
XX
XX Protein identification; signal transduction pathway; metabolic pathway;
XX hybridisation assay; genetic mapping; gene expression control; promoter;
XX termination sequence.
XX
XX Arabidopsis thaliana.
XX
XX EPI033405-A2.
XX
XX PD 06-SEP-2000.
XX
XX
XX 25-FEB-2000; 2000EP-0301439.
XX
XX
XX 25-FEB-1999; 99US-0121825.
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XX 05-MAR-1999; 99US-0123180.
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XX 09-MAR-1999; 99US-0123548.
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XX 23-MAR-1999; 99US-0125788.
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XX 25-MAR-1999; 99US-0126264.
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XX 29-MAR-1999; 99US-0126785.
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XX 01-APR-1999; 99US-0127462.
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XX 06-APR-1999; 99US-0128234.
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XX 08-APR-1999; 99US-0128714.
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XX 16-APR-1999; 99US-0129845.
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XX 07-MAY-1999; 99US-0132487.
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XX 11-MAY-1999; 99US-0132863.
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XX 19-MAY-1999; 99US-0134941.
XX
XX 20-MAY-1999; 99US-0135124.
XX
XX 21-MAY-1999; 99US-0135353.
XX
XX 24-MAY-1999; 99US-0135629.
XX
XX 25-MAY-1999; 99US-0136021.
XX
XX 27-MAY-1999; 99US-0136392.
XX
XX 28-MAY-1999; 99US-0136782.
XX
XX 01-JUN-1999; 99US-0137222.
XX
XX 03-JUN-1999; 99US-0137528.
XX
XX 04-JUN-1999; 99US-0137502.
XX
XX 07-JUN-1999; 99US-0137724.
XX
XX 08-JUN-1999; 99US-0138094.
XX
XX 10-JUN-1999; 99US-0138540.
XX
XX 10-JUN-1999; 99US-0138847.
XX
XX 14-JUN-1999; 99US-0139119.
XX
XX 16-JUN-1999; 99US-0139452.
XX
XX 16-JUN-1999; 99US-0139453.
XX
XX 17-JUN-1999; 99US-0139492.


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ID  AAU31057 standard; Protein; 229 AA.
XX
AC  AAU31057;
XX
DT  18-DEC-2001 (first entry)
XX
DE  Novel human secreted protein #1548.
XX
KM  Human; vaccination; gene therapy; nutritional supplement;
KW  stem cell proliferation; haematopoiesis; nerve tissue regeneration;
XX  immune suppression; immune stimulation; anti-inflammatory; leukaemia.
OS  Homo sapiens.
XX
PN  W0200179449-A2.
XX
PD  25-OCT-2001.
XX
PF  16-APR-2001; 2001MO-US08656.
XX
PR  18-APR-2000; 2000US-0552929.
XX  26-JAN-2001; 2001US-0770160.
XX
PA  (HYSE-) HYSEQ INC.
XX
PI  Tang YT, Liu C, Drmanac RT.
XX
DR  WPI; 2001-611725/70.
XX
PT  Nucleic acids encoding a range of human polypeptides, useful in genetic
XX  vaccination, testing and therapy -
XX
PS  Claim 20; Page 397; 765pp: English.
XX
CC  The invention relates to novel human secreted polypeptides. The
CC  polypeptides and antibodies to the polypeptides are useful for
CC  determining the presence of or predisposition to a disease associated
CC  with altered levels of polypeptide. The polypeptides are also useful for
CC  identifying agents (agonists and antagonists) that bind to them. Cells
CC  expressing the proteins are useful for identifying a therapeutic agent
CC  for use in treatment of a pathology related to aberrant expression or
CC  physiological interactions of the polypeptide. Vectors comprising
CC  the nucleic acids encoding the polypeptides and cells genetically
CC  engineered to express them are also useful for producing the proteins.
CC  The proteins are useful in genetic vaccination, testing and
CC  therapy, and can be used as nutritional supplements. They may be used to
CC  increase stem cell proliferation; to regulate haematopoiesis; and in
CC  bone, cartilage, tendon and/or nerve tissue growth or regeneration;
CC  immune suppression and/or stimulation; as anti-inflammatory agents; and
CC  in treatment of leukaemias. AAU29510-AAU3304 represent the amino acid
XX  sequences of novel human secreted proteins of the invention.
XX
SQ  Sequence 229 AA:

Query Match 32.2%; Score 19; DB 22; Length 229;
Best Local Similarity 100.0%; Pred. No. 6.4e-12;
Matches 19; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY  36 MQYRRFVNVPTEGKKKG 54
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DB  1 MQYRRFVNVPTEGKKKG 19

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